

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY**Type of Search****Vendors and cost where applicable**

Searcher: <u>P. Schrader</u>	NA Sequence (#) <u>4</u>	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: <u>Rensselaer 61A61</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/4</u>	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>14</u>	Fulltext _____	Sequence Systems <u>CompuLink</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>23</u>	Other _____	Other (specify) _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 1, 2004, 21:45:56 ; Search time 45 Seconds
(without alignments)
495.609 Million cell updates/sec

Title: US-09-866-379D-10

Perfect score: 2258
Sequence: 1 MKAILPLSLIPLTPQSA.....CSLAGTQIVNEARIPACSL 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2.6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2.6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2.6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2.6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2.6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2.6/prodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2171	96.1	440	3	US-09-259-214-2
2	2171	96.1	440	3	US-09-318-528-2
3	2171	96.1	440	3	US-09-291-931-2
4	2147	95.1	433	4	US-09-540-149A-1
5	2063.5	91.4	423	2	US-08-910-798-2
6	543	24.0	421	4	US-09-489-039A-7512
7	381	16.9	522	4	US-09-489-039A-13501
8	126	5.6	439	4	US-09-044-718-3
9	126	5.6	440	4	US-09-684-855-106
10	126	5.6	440	4	US-09-684-855-108
11	126	5.6	440	4	US-09-684-855-109
12	126	5.6	440	4	US-09-684-855-110
13	126	5.6	440	4	US-09-684-855-111
14	126	5.6	440	4	US-09-684-855-112
15	126	5.6	440	4	US-09-684-855-113
16	126	5.6	440	4	US-09-684-855-114
17	126	5.6	440	4	US-09-684-855-115
18	126	5.6	440	4	US-09-684-855-116
19	126	5.6	440	4	US-09-684-855-117
20	126	5.6	440	4	US-09-684-855-118
21	126	5.6	440	4	US-09-684-855-119
22	126	5.6	440	4	US-09-684-855-120
23	126	5.6	440	4	US-09-684-855-121
24	126	5.6	440	4	US-09-684-855-122
25	126	5.6	440	4	US-09-684-855-123
26	126	5.6	440	4	US-09-684-855-124
27	126	5.6	440	4	US-09-684-855-125

28	116	5.1	440	4	US-09-684-855-126	Sequence 131, App
29	116	5.1	440	4	US-09-684-855-127	Sequence 154, App
30	116	5.1	440	4	US-09-684-855-128	Sequence 81, App
31	109.5	4.8	465	4	US-09-044-718-81	Sequence 14, App
32	109.5	4.8	479	1	US-07-923-724-2	Sequence 2, App
33	109.5	4.8	479	2	US-08-609-426A-2	Sequence 4, App
34	109.5	4.8	479	2	US-08-374-653C-4	Sequence 142, App
35	109	4.8	413	4	US-09-684-855-142	Sequence 119, App
36	109	4.8	422	4	US-08-993-353-28	Sequence 28, App
37	109	4.8	442	3	US-09-273-871A-4	Sequence 28, App
38	109	4.8	442	4	US-09-482-558A-28	Sequence 14, App
39	109	4.8	442	4	US-09-636-499-14	Sequence 14, App
40	108.5	4.8	455	4	US-08-758-213-1	Sequence 1, App
41	108	4.8	386	2	US-08-692-787-48	Sequence 48, App
42	108	4.8	386	2	US-09-097-199-48	Sequence 2, App
43	108	4.8	386	2	US-09-146-283-2	Sequence 48, App
44	108	4.8	515	2	US-08-579-823A-2	Sequence 2, App
45	108	4.8	515	3	US-08-579-823A-2	Sequence 2, App

ALIGNMENTS

RESULT 1	US-09-259-214-2	Application US/09259214A
Sequence 2, Appli	Patent No. 6110719	
GENERAL INFORMATION:		
APPLICANT: Kretz, Keith		
TITLE OF INVENTION: NOVEL PHYTASE		
FILE REFERENCE: DIVER1370-1		
CURRENT FILING DATE: 1999-03-01		
EARLIER APPLICATION NUMBER: 08/910,798		
EARLIER FILING DATE: 1997-08-13		
NUMBER OF SEQ ID NOS: 4		
SOFTWARE: FastSeq for Windows Version 4.0		
SEQ ID NO 2		
LENGTH: 440		
TYPE: PRT		
ORGANISM: Escherichia coli		
US-09-259-214-2		
Query Match	96.1%; Score 2171; DB 3; Length 440;	
Best Local Similarity	97.7%; Pred. No. 4.4e-221;	
Matches 422; Conservative	0; Mismatches 10; Indels 0; Gaps 0;	
QY	1	1
DB	1	1
QY	61	61
DB	61	61
QY	121	121
DB	121	121
QY	181	181
DB	181	181
QY	241	241
DB	241	241
QY	301	301
DB	301	301
QY	361	361
DB	361	361

Db 361 RRLSDNSQWIOVSLVFTQLQOMRDKTPLSLNTPPGEVKLTLAGCEBNNAGMCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432

RESULT 2
US-09-318-528-2
Sequence 2, Application US/09318528
Patent No. 6183740
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
TYPE: PRT
ORGANISM: Escherichia coli
US-09-318-528-2

Query Match 96.1%; Score 2171; DB 3; Length 440;
Best Local Similarity 97.7%; Pred. No. 4,4e-221;
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKAIIIPFSLIPLTPQSAFAQSEBELKLESVIVSRGVAPTKATQLMQDVTDPDAMP 60
Db 1 MKAIIIPFSLIPLTPQSAFAQSEBELKLESVIVSRGVAPTKATQLMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGELIAYIGHYRQRLVADGLPKKCGPQSGQVAIIVADVETRTKGE 120
Db 61 TWPVKLGELTPRGELIAYIGHYRQRLVADGLPKKCGPQSGQVAIIVADVETRTKGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVQCLDANANTDAILERAGSIAIDFTGH 180
Db 121 APAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVQCLDANANTDAILERAGSIAIDFTGH 180
QY 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240
Db 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240
QY 241 EIFLLOQAQMPPEPGGRITDSHQNTLLSLHNAQFDLQRTPEVARSATPLDLIMXA 300
Db 241 EIFLLOQAQMPPEPGGRITDSHQNTLLSLHNAQFDLQRTPEVARSATPLDLIMXA 300
QY 301 LTFHPPOKQAYGTLTPSVLFIAGHDTNLANLGALFLNWTLPQCPDNTPPGGEIVFERM 360
Db 301 LTFHPPOKQAYGTLTPSVLFIAGHDTNLANLGALFLNWTLPQCPDNTPPGGEIVFERM 360
QY 361 RRLSDNSQWIOVSLVFTQLQOMRDKTPLSLNTPPGEVKLTLAGCEBNNAGMCSLAGFTQ 420
Db 361 RRLSDNSQWIOVSLVFTQLQOMRDKTPLSLNTPPGEVKLTLAGCEBNNAGMCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432

RESULT 3
US-09-291-931-2
Sequence 2, Application US/09291931A
Patent No. 6190897
GENERAL INFORMATION:

APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
TYPE: PRT
ORGANISM: Escherichia coli
US-09-291-931-2

Query Match 96.1%; Score 2171; DB 3; Length 440;
Best Local Similarity 97.7%; Pred. No. 4,4e-221;
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKAIIIPFSLIPLTPQSAFAQSEBELKLESVIVSRGVAPTKATQLMQDVTDPDAMP 60
Db 1 MKAIIIPFSLIPLTPQSAFAQSEBELKLESVIVSRGVAPTKATQLMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGELIAYIGHYRQRLVADGLPKKCGPQSGQVAIIVADVETRTKGE 120
Db 61 TWPVKLGELTPRGELIAYIGHYRQRLVADGLPKKCGPQSGQVAIIVADVETRTKGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVQCLDANANTDAILERAGSIAIDFTGH 180
Db 121 APAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVQCLDANANTDAILERAGSIAIDFTGH 180
QY 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240
Db 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240
QY 241 EIFLLOQAQMPPEPGGRITDSHQNTLLSLHNAQFDLQRTPEVARSATPLDLIMXA 300
Db 241 EIFLLOQAQMPPEPGGRITDSHQNTLLSLHNAQFDLQRTPEVARSATPLDLIMXA 300
QY 301 LTFHPPOKQAYGTLTPSVLFIAGHDTNLANLGALFLNWTLPQCPDNTPPGGEIVFERM 360
Db 301 LTFHPPOKQAYGTLTPSVLFIAGHDTNLANLGALFLNWTLPQCPDNTPPGGEIVFERM 360
QY 361 RRLSDNSQWIOVSLVFTQLQOMRDKTPLSLNTPPGEVKLTLAGCEBNNAGMCSLAGFTQ 420
Db 361 RRLSDNSQWIOVSLVFTQLQOMRDKTPLSLNTPPGEVKLTLAGCEBNNAGMCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432

RESULT 4
US-09-540-149A-1
Sequence 1, Application US/09540149A
Patent No. 651699
GENERAL INFORMATION:
APPLICANT: Lei, Xiangen
TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 433
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:

Tue May 4 07:05:29 2004

us-09-866-379d-10.ra1

Page 3

NAME/KEY: UNSURE
LOCATION: (433)
OTHER INFORMATION: Xaa at position 433 in this sequence is unknown
US-09-540-149A-1

Query Match 95.1%; Score 2147; DB 4; Length 433;
Best Local Similarity 96.8%; Pred. No. 1.5e-218;
Matches 418; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKALIFPLSLIPLTPQSAFQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60
DB 1 MKALIFPLSLIPLTPQSAFQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60
QY 61 TWPVKGELTPRGELIAYLGHYRQRLVADGLPKCGCQSGQVAILADVDETRKTGE 120
DB 61 TWPVKGELTPRGELIAYLGHYRQRLVADGLPKCGCQSGQVAILADVDETRKTGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDPLFNPDKTGVQCLDNANVTDAILSRAGSIADEFTGH 180
DB 121 APAAGLAPDCAITVHTQADTSSPDPLFNPDKTGVQCLDNANVTDAILSRAGSIADEFTGH 180
QY 181 YOTAFRELERVNFPSQNLCKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
DB 181 ROTAFRELERVNFPSQNLCKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
QY 241 EIFLLQQAQMPGPGKGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 300
DB 241 EIFLLQQAQMPGPGKGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 300
QY 301 LTPHPKQKAYGVTLPTSVLFIAGHDNTLANLGALIELNMTLPQGDNTPPGSELVFERM 360
DB 301 LTPHPKQKAYGVTLPTSVLFIAGHDNTLANLGALIELNMTLPQGDNTPPGSELVFERM 360
QY 361 RLSDNSQMIQVSLVFTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 420
DB 361 RLSDNSQMIQVSLVFTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432

RESULT 5
US-08-910-798-2
Sequence 2, Application US/08910798
Patent No. 5876997
GENERAL INFORMATION:
APPLICANT: KREITZ
TITLE OF INVENTION: NOVEL PHRYASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-798-2

Query Match 91.4%; Score 2063.5; DB 2; Length 423;
Best Local Similarity 93.8%; Pred. No. 1e-209;
Matches 405; Conservative 0; Mismatches 10; Indels 17; Gaps 1;

QY 1 MKALIFPLSLIPLTPQSAFQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60
DB 1 MKALIFPLSLIPLTPQSAFQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60
QY 61 TWPVKGELTPRGELIAYLGHYRQRLVADGLPKCGCQSGQVAILADVDETRKTGE 120
DB 61 TWPVKGELTPRGELIAYLGHYRQRLVADGLPKCGCQSGQVAILADVDETRKTGE 119
QY 121 APAAGLAPDCAITVHTQADTSSPDPLFNPDKTGVQCLDNANVTDAILSRAGSIADEFTGH 180
DB 120 -----QADTSSPDPLFNPDKTGVQCLDNANVTDAILSRAGSIADEFTGH 163
QY 181 YOTAFRELERVNFPSQNLCKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
DB 164 ROTAFRELERVNFPSQNLCKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 223
QY 241 EIFLLQQAQMPGPGKGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 300
DB 224 EIFLLQQAQMPGPGKGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 283
QY 301 LTPHPKQKAYGVTLPTSVLFIAGHDNTLANLGALIELNMTLPQGDNTPPGSELVFERM 360
DB 284 LTPHPKQKAYGVTLPTSVLFIAGHDNTLANLGALIELNMTLPQGDNTPPGSELVFERM 343
QY 361 RLSDNSQMIQVSLVFTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 420
DB 344 RLSDNSQMIQVSLVFTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 403
QY 421 IYNEARIPACSL 432
DB 404 IYNEARIPACSL 415

RESULT 6
US-09-489-039A-7512
Sequence 7512, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7512
LENGTH: 421
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7512
Query Match 24.0%; Score 543; DB 4; Length 421;
Best Local Similarity 32.6%; Pred. No. 1.1e-48;
Matches 136; Conservative 70; Mismatches 181; Indels 30; Gaps 10;
QY 19 SAGAFQSE----PE-LKESVIVSRHGVRAP-TKATQMODVTPDAMPPTVPLGELTPR 72
DB 23 SAGAFQSEKAPBEQYLOQVYLIMSRLHRLAPLANNGSVLEOSTAKAWPQMDVPGGLTTK 82

QY 73 GGEIAYIGHYWRQRLVADGILPKCGCGSGVAVIADVERTRTKGTGAFAAGIAPDCAI 132
 DB 83 GGVELEVYNGHWRRELAQOKLVTSGCEPPENAVAVANSIQRIVATAQFFITGAFFCGGI 142
 QY 133 THTQADTSSPDLFENPLKGTGVCQJDNANVTDAI-LEBAGSIAIDFTGHYQTAFRELERV 191
 DB 143 PVHHPQMGCTMDPTNPVITDSDSPAFREKALQAMKEKQGMQULR-----SKLEFTM 195
 QY 192 LNFPGSNCLKREKODESCSLTQALPSBLKVADCVSLTGAVSLSMTEIFLLQQAQGM 251
 DB 196 IDYRNSPEC---KEKVKYCSLSEKDTFSAGYQCEPVGSGPLKVNISIVDAFTIQQYEYGF 251
 QY 252 P--EENGGRITDSHOMNTLLSLHNAQFDLQRTPEVARSRAATPLLDIKTLTTHPPOKQ 309
 DB 252 PDDQVANKGEIASDKMRYLSKIKGYQDSLFTSVAVNAQVAKPLVKYIDNALVGBGASK- 310
 QY 310 AYGVTLPTSGLFIAGHDNTLANLGGALBLN-WTLPGQPDNTPPGGELVEFERMRSLSDNSQ 368
 DB 311 -----AKVTLVGHDSNISILTLALDPKPYQLPGQYERTPIGGKLLFORHDSAGNRD 363
 QY 369 WIOVSLVFQTLQOMKDKTPISLNTPPGEVKLTLAGCEERNAGMCSLAGTQIVNEA 425
 DB 364 LMKIYVYQSTQJOLNADALTIQAPFORVTLALNGCPV-DIOGFCPLETFKXVINEA 419

RESULT 7

US-09-489-039A-13501
 ; Sequence 13501, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13501
 ; LENGTH: 522
 ; TYPE: PRD
 ; ORGANISM: Klebsiella pneumoniae
 ; US-09-489-039A-13501

Query Match 16.9%; Score 381; DB 4; Length 522;
 Best Local Similarity 26.3%; Pred. No. 2.3e-31;

Matches 117; Conservative 73; Mismatches 209; Indels 46; Gaps 15;

QY 2 KAILPPLSLPLPLP-OSAPFQSEPELKLSEVIVSRHGVAPKAI-QLMQDVTTPAW 59
 DB 107 QGLHLPLTACALPLALQSAHA---ADWQLEKVALSHHGLRPPAGREKALTEATGRFW 163
 QY 60 PTWPYKLGELPRGSELIAVLGHYWRQRLVADGILPKCGCGSGVAVIADVERTRTKGT 119
 DB 164 TWTHTHDEGLGHYAALVNNKGRAGQHYRQGLL-QAGCPTASIIYVRAAPLQRTATA 222
 QY 120 EAPFAGLAPDCAITVHTQADTSSPDLFENPLKGTGVCQJDNANVTDAI-LEBAGSIAIDFTG 179
 DB 223 QALVDGAFPGCVAAHYV--SGDADPLFQTDKFAATQTDPAKQLAAVEKKG---DLAQ 276
 QY 180 HYQTAFRELERVLANFPOSNCLKREKODESCSLTQALPSBLKVADCVSLTGAVSLSMTE 239
 DB 277 RRGQ----LAPTIQLKQAVC---QADKPCPIPT-PMQVQSGSKGTTISGLSVAMN 327
 QY 240 TEIFLLQQAQGM--EPGGRITDSDHOMNTLLSLHNAQFDLQRTPEVARSRAATPLLDLI 297
 DB 328 VETLRIGSENPLSLQALWAKITQARQITALLPLLTENYDNLVYTAQKGSVLLNAM 387
 QY 298 KTAALPHPEOKQAYVTLPTSGLFIAGHDNTLANLGGALBLNMTLPG-QPDNTPPGGELV 356
 DB 388 LDGVVPEANPNVRW-----LLVADHTNIAVRTILNPSWQLPGVSRGNIPPGSSLV 439

QY 357 FERWRSLNSQMIQVSLVFQTLQOMKDKTPISLNTPPGEVKLT-----LAGCEERNAG 411
 DB 440 LERWRNASKGERYLRVYFQAQGLDILR-----RLQTPAQHMLRQEMHQPQCRQTDVGT 494
 QY 412 MC-----SLAGTQIVNEARIPACSL 432
 DB 495 LCPFOAITALQGRIDRSSAPAYAM 519

RESULT 8

US-09-044-718-3
 ; Sequence 3, Application US/09044718
 ; Patent No. 6391605
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTREMA, Dirk
 ; APPLICANT: PASAMONTES, Luis
 ; APPLICANT: TOMSCHY, Andrea
 ; APPLICANT: van LOON, Adolphus
 ; APPLICANT: VOGEL, Kurt
 ; APPLICANT: WYSS, Markus
 ; TITLE OF INVENTION: MODIFIED PHYTASES
 ; FILE REFERENCE: Modified Phytases
 ; CURRENT APPLICATION NUMBER: US/09/044,718
 ; CURRENT FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: EP 97810175.6
 ; PRIOR FILING DATE: 1997-03-25
 ; NUMBER OF SEQ ID NOS: 82
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 439
 ; TYPE: PRD
 ; ORGANISM: Aspergillus fumigatus
 ; US-09-044-718-3

Query Match 5.6%; Score 126; DB 4; Length 439;
 Best Local Similarity 20.9%; Pred. No. 0.00017;
 Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPQSAFQSEPELKLSEVIVSRHGVAPF-----KATQIMQDVTDA--- 58
 DB 26 PFLSLDELVSLSKLPK--DCRITLVQVLSRHGRARPPSSKSKYKYLVTALQANATDF 82
 QY 59 -----WPTWPYKLG--ELTPRGSELIAVLG--HYWRQRLVADGILPKCGCGSGVAVI 108
 DB 83 KGRFAPLKYNNYTLGADDLTPRGEGQLVNSGIKTYQRYKALRSVP-----FIR 132
 QY 109 ADVDETRTKGEAFAGL-----APDCAITVHTQADTSSPDLFENPLKGTG 154
 DB 133 AGSDRVIASGEKFIQFOAKLADPGATNRAAPALSVII--DESEFN-----NTLDHGV 186
 QY 155 C-QJDNANVTDALEBAGSIAIDFTGHYQTAFRELERVLANFPOSNCLKREKODESCSLT 213
 DB 187 CTKEFASQADEV-----ANFTALFPADIR-----AAAEKH----- 218
 QY 214 QALPSELKVSADCVSLTGAVSLSMTEIFLLQQAQGMPEGMGRITDSDHOMNTLLSL- 271
 DB 219 --LPGVTLDEBDVYSLMDKSPDTV-----ARTSDASQLSPFQCLPT 258
 QY 272 HN--AQFDLQ-----TPS-VARSRAATPLLDIKT--ALTPRP 305
 DB 259 HNMWKXNYNLIQSLGKYYGYGAGNPLGPAQIGFTMELIARLRSVPQDHTSTNSTLVSNP 318
 QY 306 POKQAYVTLPTSGLFI--GHDTNLANLGGALBLNMTLPGQPDNTPPGGELVFERMRSL 363
 DB 319 -----ATPPLNATMYVVPFSHNSVSLFPAL-----GLYNGTEPLSTSVESAKEL 364
 QY 364 SD-NSQMT---QVSLVFQTLQOMKDKTPISLNTPPGEVKLTLAGCEERNAGMCSLAGT 419
 DB 365 DGYSASVVPFGARAVETMQCKSEKPL-VRALINDRVVPLHGCIV-DKIGRCKLNDIV 422
 QY 420 QIVNEAR 426
 DB 423 KGLSMAR 429

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RESULT 9
US-09-684-855-106
; Sequence 106, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/11692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 106
; LENGTH: 440
; TYPE: PRF
; ORGANISM: A. fumigatus 13073
US-09-684-855-106

Query Match      5.6%; Score 126; DB 4; Length 440;
Best Local Similarity 20.9%; Pred. No. 0.00017;
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPGSAFAQSEBELKLESVIVSRHGVRAPT-----KATQLMQDVTTPDA--- 58
DB 27 PFLSLEDELSTVSSKLPK---DCRITLVQVLSRHGARYPTSSKSKYKLVTAIQANATDF 83
QY 59 -----WPTWPKVG--ELTPRGGEIAYIG--HYRKQRLVADGLPKGCGPQSGQVAII 108
DB 84 KGRKPAFLKTYNTLTGADDLTPFGHQQLVNSGIRFYQRYKALARSVP-----FIR 133
QY 109 ADVDETRTKTGEAFPAAGL-----APDCAITVHTQADTSSPDPLFNPKTGIV 154
DB 134 ASGSDRIYASGEKFTIEGFOQAKLADPGATNRAAPAIISVII--PESETFN-----NTLDHGV 187
QY 155 C-QLDNANVTDAILERAGGSIADFTGHYQTAPELELRVINFPOSNI-CKREKQDESCSLT 213
DB 188 CTKEFAAQQLDEV-----AANFTALFAPDIR-----ARAEKH----- 219
QY 214 QALPSELKVASDVCSTLGAVALSMLTEIFLLQQAQMPERPGWGRITDSHQNTLLSL-- 271
DB 220 --LPGVTLTDEDEVVSLMDMCSFDTV-----ARTSDASQLSPFQQLFT 259
QY 272 HN--AQFDLLQK-----TPE-VASRATPLLDLTKT--ALTHPH 305
DB 260 HNEWKKNYVLSQSLGKYYGAGNPLGPAQIGFTNELIARLRSPODHTSTNSTLVSNP 319
QY 306 POKQAYGVTLPTSLVFLA--GHDITNLANLGGALBELNMTLPGQPDNTPPGSELVFERMRRL 363
DB 320 -----ATFPLNATWYVDFSHDMSWVSIFPAL-----GLYNGTEPLSRTSVESAKEL 365
QY 364 SD-NSQWIT---QVSLVFQTLQOMRDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFT 419
DB 366 DGYASWVVPFGARAYETWQCKSEKEPL--VRALLINDRVVPLHGDV--DGLGRCKLNDPV 423
QY 420 QIVNEAR 426
DB 424 KGLSWAR 430

RESULT 10
US-09-684-855-128
; Sequence 128, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/11692
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US-09-684-855-106
; Sequence 106, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/11692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 151
; LENGTH: 440

Query Match      5.6%; Score 126; DB 4; Length 440;
Best Local Similarity 20.9%; Pred. No. 0.00017;
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPGSAFAQSEBELKLESVIVSRHGVRAPT-----KATQLMQDVTTPDA--- 58
DB 27 PFLSLEDELSTVSSKLPK---DCRITLVQVLSRHGARYPTSSKSKYKLVTAIQANATDF 83
QY 59 -----WPTWPKVG--ELTPRGGEIAYIG--HYRKQRLVADGLPKGCGPQSGQVAII 108
DB 84 KGRKPAFLKTYNTLTGADDLTPFGHQQLVNSGIRFYQRYKALARSVP-----FIR 133
QY 109 ADVDETRTKTGEAFPAAGL-----APDCAITVHTQADTSSPDPLFNPKTGIV 154
DB 134 ASGSDRIYASGEKFTIEGFOQAKLADPGATNRAAPAIISVII--PESETFN-----NTLDHGV 187
QY 155 C-QLDNANVTDAILERAGGSIADFTGHYQTAPELELRVINFPOSNI-CKREKQDESCSLT 213
DB 188 CTKEFAAQQLDEV-----AANFTALFAPDIR-----ARAEKH----- 219
QY 214 QALPSELKVASDVCSTLGAVALSMLTEIFLLQQAQMPERPGWGRITDSHQNTLLSL-- 271
DB 220 --LPGVTLTDEDEVVSLMDMCSFDTV-----ARTSDASQLSPFQQLFT 259
QY 272 HN--AQFDLLQK-----TPE-VASRATPLLDLTKT--ALTHPH 305
DB 260 HNEWKKNYVLSQSLGKYYGAGNPLGPAQIGFTNELIARLRSPODHTSTNSTLVSNP 319
QY 306 POKQAYGVTLPTSLVFLA--GHDITNLANLGGALBELNMTLPGQPDNTPPGSELVFERMRRL 363
DB 320 -----ATFPLNATWYVDFSHDMSWVSIFPAL-----GLYNGTEPLSRTSVESAKEL 365
QY 364 SD-NSQWIT---QVSLVFQTLQOMRDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFT 419
DB 366 DGYASWVVPFGARAYETWQCKSEKEPL--VRALLINDRVVPLHGDV--DGLGRCKLNDPV 423
QY 420 QIVNEAR 426
DB 424 KGLSWAR 430

RESULT 11
US-09-684-855-151
; Sequence 151, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/11692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 151
; LENGTH: 440
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 119
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 228
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 337
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-866-435-33

Query Match 5.6%; Score 126; DB 3; Length 465;
Best Local Similarity 20.9%; Pred. No. 0.00019;
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

7 PFLSLIPLTPQSAFQSEBELKESVIVSRHGVRAPI-----KATOLMDVTPDA--- 58
52 PFLSLIPLTPQSAFQSEBELKESVIVSRHGVRAPI-----KATOLMDVTPDA--- 108
59 -----WPTWPKLG--ELTPRGELIAYLG--HYRQQLVADGELPKCGQSGQVAII 108
109 KGFPAFLKTYNTLTGADLTLPGEQQLVNSGIRKFORVYALRSVVP-----FIR 158
109 ADVDERTRKTGEAFAGL-----APDCATVHQADTSSPDLFNLKTV 154
159 ASGSDVIVASGEKTEGFGQALADPGATNRAAPALSVII-PESETFN-----NTLDHGV 212
155 C-QLDNNAVYTDALIERAGSIAIDFTGHQYAFRELERVLPQSNICLREKODESCSLT 213
213 CTKEFASQIGDEV-----ANFTALFAPDIR-----ARAEKQ----- 244
214 QALPBEIKYSACVSTIGAVSLASMLTEFLQQAQMPGEMGRITLISHONTLLSL-- 271
245 --LPGVTLTDEBYVSLMDKCSFDIV-----ARTSDSQSLSPCQLFT 284
272 HN--AQFDLLQR-----TPE-VARSRAATPLDLIKT--ALTRHP 305
285 HNEWKKYNVLQSLGKYYGAGNPLGPAQIGFTVHLLARLTRSPQDHTSTNSLTVSNP 344
306 POKQAVGLTFLPSVFLIA--GHDNTLANIGALMLNWTLPQGPDMTPPGDELVFERKRL 363
345 -----APFPINATMYVDFSHNSVVSIFPAL-----GLYNGTEPLSRITSVAHEL 390
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391 DGSAASAVVVPFGARAFETMCKSEKPL-VRALINDRVVPLHGCV-DKGRCLNDLV 448
420 QIVNEAR 426
449 KGLSMAR 455

RESULT 14
US-08-744-231-33
Sequence 33; Application US/08744231
Patent No. 6358722
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: POLYPEPTIDES WITH PHRYASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kaas, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 119
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US-08-744-231-33

Query Match 5.6%; Score 126; DB 4; Length 465;
Best Local Similarity 20.9%; Pred. No. 0.00019;
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;
7 PFLSLIPLTPQSAFQSEBELKESVIVSRHGVRAPI-----KATOLMDVTPDA--- 58


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Db      52 PFFSLEDELVSXSKLPK---DCRITLVQVLRSRGARVPTSSKSKYKLVTAIAQANATDF 108
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Db      109 KGRFAFLKTYNTLTGADDLTPFGHQQLVNSGIKFYQRYKALARSVP-----FIR 158
Qy      109 ADVDERTRKTGEAFPAAGL-----APDCATVHTQADTSSPDPPLFNPKTG 154
Db      159 ASGSDRVIASGEKFTIEGFOQAKLADPGATNRAAPALISVII-PSEFTN-----NTLDHGV 212
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Db      213 CTKEBASQLGDEV-----AANFTALFAPDIR-----ARAEKH----- 244
Qy      214 QALPSELKVSADCVSLTGAVALSMLEIFLLQQAQMPFGWRGRTDTSQWNTLSL-- 271
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Db      285 HNEWKXNYLQSLGKYGYGAGNPLGPAQIGFTNELIARITRSPVODHTSTNSTIVSNP 344
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RESULT 15

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US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

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Query Match      5.6%; Score 126; DB 4; Length 465;
Best Local Similarity 20.9%; Pred. No. 0.00019;
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

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Qy      7 PFLSLIPLTPQSAFAQSEPELKSIVLVSRHGVRAPT-----KATQIMODVTPDA-- 58
Db      52 PFFSLEDELVSXSKLPK---DCRITLVQVLRSRGARVPTSSKSKYKLVTAIAQANATDF 108
Qy      59 -----WPTWPKVLG--ELTPRGELIAYIG--HYRQRLVADGLPKGCCPGSGVAILI 108
Db      109 KGRFAFLKTYNTLTGADDLTPFGHQQLVNSGIKFYQRYKALARSVP-----FIR 158
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Db      213 CTKEBASQLGDEV-----AANFTALFAPDIR-----ARAEKH----- 244
Qy      214 QALPSELKVSADCVSLTGAVALSMLEIFLLQQAQMPFGWRGRTDTSQWNTLSL-- 271
Db      245 --LPGVTLTDEVDVSLMDMCSFDTV-----ARTSDAQLSPPCQLFT 284
Qy      272 HN--AQEDLLQR-----TPE-VASBRATPLDLIKT--ALTEHP 305
Db      285 HNEWKXNYLQSLGKYGYGAGNPLGPAQIGFTNELIARITRSPVODHTSTNSTIVSNP 344
Qy      306 PQKQAVGVTLPSTVLFIA--GHDTNLANLGALBLNMTLPGQPNTPPGSELVFERWRRL 363
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Qy      364 SD-NSQWT---QVSLVFQTLQOMRDKTPLSINTPPGEVKLTLAGCEERNAGMCSLAGFT 419
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Qy      420 QIVNEAR 426
Db      449 KGLSWAR 455

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GenCore version 5.1.6
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Title: US-09-866-379D-10

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Minimum DB seq length: 0
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Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2182	96.6	432	9	US-09-866-379-8
4	2182	96.6	432	12	US-10-282-122A-43351
5	2182	96.6	432	14	US-10-156-660-4
6	2171	96.1	440	9	US-09-777-566A-2
7	2171	96.1	440	9	US-09-866-379-2
8	2171	96.1	440	14	US-10-034-985-2
9	2171	96.1	440	15	US-10-430-356-2
10	2157	95.5	412	14	US-10-334-672-1
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15	2147	95.1	432	15	US-10-284-962-14

16	2147	95.1	433	14	US-10-266-041-1	Sequence 1, Appli
17	2144	95.0	432	15	US-10-284-962-5	Sequence 5, Appli
18	2112	93.5	432	14	US-10-021-723A-16	Sequence 16, Appl
19	976.5	43.2	441	14	US-10-021-723A-12	Sequence 12, Appl
20	959.5	42.5	441	12	US-10-282-122A-77792	Sequence 2, Appli
21	951.5	42.1	441	14	US-10-021-723A-2	Sequence 4, Appli
22	948.5	42.0	441	14	US-10-021-723A-4	Sequence 10, Appl
23	782	34.6	416	14	US-10-021-723A-10	Sequence 14, Appl
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26	462.5	20.5	421	14	US-10-021-723A-6	Sequence 44, Appl
27	197	8.7	426	12	US-10-257-174-44	Sequence 6, Appli
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29	126	5.6	439	14	US-10-063-848-3	Sequence 106, App
30	126	5.6	440	12	US-10-442-538-106	Sequence 128, App
31	126	5.6	440	12	US-10-442-538-128	Sequence 151, App
32	126	5.6	440	12	US-10-442-538-151	Sequence 12, Appl
33	126	5.6	449	14	US-10-062-848-12	Sequence 8, Appli
34	126	5.6	465	13	US-10-063-452-8	Sequence 78, Appl
35	126	5.6	465	14	US-10-062-848-78	Sequence 6, Appli
36	126	5.6	465	14	US-10-229-358-6	Sequence 24, Appl
37	126	5.6	474	14	US-10-213-980-24	Sequence 107, App
38	125	5.5	440	12	US-10-442-538-107	Sequence 125, App
39	125	5.5	440	12	US-10-442-538-129	Sequence 152, App
40	125	5.5	440	12	US-10-442-538-152	Sequence 165, App
41	124	5.5	467	12	US-10-442-538-165	Sequence 59099, A
42	122.5	5.4	99	12	US-10-282-132A-59099	Sequence 108, App
43	118	5.2	440	12	US-10-442-538-108	Sequence 130, App
44	118	5.2	440	12	US-10-442-538-130	Sequence 153, App
45	118	5.2	440	12	US-10-442-538-153	

ALIGNMENTS

RESULT 1
US-10-156-660-2
Sequence 2, Application US/10156660
Publication No. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Eileen
TITLE OR INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
TITLE OR INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US/10/156,660
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 436
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified phytase enzyme
US-10-156-660-2

Query Match 100.0%; Score 2258; DB 14; Length 436;
 Best Local Similarity 100.0%; Pred. No. 3,8e-208;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAILPILSLILPLTPQSAFAQSEPELKLESVIVSRHGVRAPTATQTMQVTPDAMP 60
 DB 1 MKAILPILSLILPLTPQSAFAQSEPELKLESVIVSRHGVRAPTATQTMQVTPDAMP 60

QY 61 TWPVKLGELTRPGGELLAYLGHYWRQRLVADGLPKGCGPQSGQVAILADVDETRKTGE 120
 DB 61 TWPVKLGELTRPGGELLAYLGHYWRQRLVADGLPKGCGPQSGQVAILADVDETRKTGE 120

QY 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPPLKTVGCOLDNANVTDAILERAGSIAIDFTGH 180
 DB 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPPLKTVGCOLDNANVTDAILERAGSIAIDFTGH 180

QY 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPPLKTVGCOLDNANVTDAILERAGSIAIDFTGH 180
 DB 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPPLKTVGCOLDNANVTDAILERAGSIAIDFTGH 180

QY 181 YQTAFREIERLVNFPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
 DB 181 YQTAFREIERLVNFPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

QY 241 EIFLLQQAQGMPEPQMGRIITDSHOMNTLLSLHNAQFDLQRTPEVARSATPLLDLIXTA 300
 DB 241 EIFLLQQAQGMPEPQMGRIITDSHOMNTLLSLHNAQFDLQRTPEVARSATPLLDLIXTA 300

QY 301 LTPHPQKQAYGVTLPSTVLFIAHDNTLANLGGALBLNMTLPQGPNTTPGGELVFERW 360
 DB 301 LTPHPQKQAYGVTLPSTVLFIAHDNTLANLGGALBLNMTLPQGPNTTPGGELVFERW 360

QY 361 RLSDNSQWICVSLVFTQLQGMKDTPLSLNTPPGEVYLTLAGCEERNAQMGSLAGFTQ 420
 DB 361 RLSDNSQWICVSLVFTQLQGMKDTPLSLNTPPGEVYLTLAGCEERNAQMGSLAGFTQ 420

QY 421 IVNEARIPACSL 432
 DB 421 IVNEARIPACSL 432

RESULT 2
 US-09-866-379-10
 ; Sequence 10, Application US/09866379
 ; Patent No. US20020136754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: SHORT, Jay
 ; APPLICANT: KREITZ, Keith
 ; APPLICANT: GRAY, Kevin
 ; APPLICANT: BARTON, Nelson
 ; APPLICANT: GARRETT, James
 ; APPLICANT: O'DONOGHUE, Eileen
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
 ; FILE REFERENCE: DIVER1370-7
 ; CURRENT APPLICATION NUMBER: US/09/866,379
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: US 09/580,515
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 09/318,528
 ; PRIOR FILING DATE: 1999-05-25
 ; PRIOR APPLICATION NUMBER: US 09/291,931
 ; PRIOR FILING DATE: 1999-04-13
 ; PRIOR APPLICATION NUMBER: US 09/259,214
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: US 08/910,798
 ; PRIOR FILING DATE: 1997-08-13
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Modified phybase
 ; US-09-866-379-10

Query Match 98.7%; Score 2228; DB 9; Length 430;
 Best Local Similarity 99.5%; Pred. No. 2,8e-205;
 Matches 430; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKAILPILSLILPLTPQSAFAQSEPELKLESVIVSRHGVRAPTATQTMQVTPDAMP 60
 DB 1 MKAILPILSLILPLTPQSAFAQSEPELKLESVIVSRHGVRAPTATQTMQVTPDAMP 60

QY 61 TWPVKLGELTRPGGELLAYLGHYWRQRLVADGLPKGCGPQSGQVAILADVDETRKTGE 120
 DB 61 TWPVKLGELTRPGGELLAYLGHYWRQRLVADGLPKGCGPQSGQVAILADVDETRKTGE 120

QY 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPPLKTVGCOLDNANVTDAILERAGSIAIDFTGH 180
 DB 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPPLKTVGCOLDNANVTDAILERAGSIAIDFTGH 179

QY 181 YQTAFREIERLVNFPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
 DB 180 YQTAFREIERLVNFPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 239

QY 241 EIFLLQQAQGMPEPQMGRIITDSHOMNTLLSLHNAQFDLQRTPEVARSATPLLDLIXTA 300
 DB 240 EIFLLQQAQGMPEPQMGRIITDSHOMNTLLSLHNAQFDLQRTPEVARSATPLLDLIXTA 298

QY 301 LTPHPQKQAYGVTLPSTVLFIAHDNTLANLGGALBLNMTLPQGPNTTPGGELVFERW 360
 DB 299 LTPHPQKQAYGVTLPSTVLFIAHDNTLANLGGALBLNMTLPQGPNTTPGGELVFERW 358

QY 361 RLSDNSQWICVSLVFTQLQGMKDTPLSLNTPPGEVYLTLAGCEERNAQMGSLAGFTQ 420
 DB 359 RLSDNSQWICVSLVFTQLQGMKDTPLSLNTPPGEVYLTLAGCEERNAQMGSLAGFTQ 418

QY 421 IVNEARIPACSL 432
 DB 419 IVNEARIPACSL 430

RESULT 3
 US-09-866-379-8
 ; Sequence 8, Application US/09866379
 ; Patent No. US20020136754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: SHORT, Jay
 ; APPLICANT: KREITZ, Keith
 ; APPLICANT: GRAY, Kevin
 ; APPLICANT: BARTON, Nelson
 ; APPLICANT: GARRETT, James
 ; APPLICANT: O'DONOGHUE, Eileen
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
 ; FILE REFERENCE: DIVER1370-7
 ; CURRENT APPLICATION NUMBER: US/09/866,379
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: US 09/580,515
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 09/318,528
 ; PRIOR FILING DATE: 1999-05-25
 ; PRIOR APPLICATION NUMBER: US 09/291,931
 ; PRIOR FILING DATE: 1999-04-13
 ; PRIOR APPLICATION NUMBER: US 09/259,214
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: US 08/910,798
 ; PRIOR FILING DATE: 1997-08-13
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-09-866-379-8

Query Match 96.6%; Score 2182; DB 9; Length 432;

Best Local Similarity 98.1%; Pred. No. 7.6e-201;
Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLTPQSAFAQSEPELKLSESVIVSRHGVRAPTKATQMLQMDVTPDAMP 60
1 MKAILIPFLSLIPLTPQSAFAQSEPELKLSESVIVSRHGVRAPTKATQMLQMDVTPDAMP 60

Db 61 TWPVKLGELTPRGSELIAVIGHYWRQRLVADGLPKCCGCPQSGQVAIIADVDERTKXGE 120
61 TWPVKLGELTPRGSELIAVIGHYWRQRLVADGLPKCCGCPQSGQVAIIADVDERTKXGE 120

QY 121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180
121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180

Db 121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180
121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180

QY 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

Db 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

QY 241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300
241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300

Db 241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300
241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300

QY 301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360
301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360

Db 301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360
301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360

QY 361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420
361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420

Db 361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420
361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420

QY 421 IVNEARIPACSL 432
421 IVNEARIPACSL 432

Db 421 IVNEARIPACSL 432
421 IVNEARIPACSL 432

RESULT 4
US-10-282-122A-43351
Sequence 43351, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykand, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITR.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 43351
LENGTH: 432
TYPE: PRF
ORGANISM: Escherichia coli
US-10-282-122A-43351

Query Match 96.6%; Score 2182; DB 12; Length 432;
Best Local Similarity 98.1%; Pred. No. 7.6e-201;
Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLTPQSAFAQSEPELKLSESVIVSRHGVRAPTKATQMLQMDVTPDAMP 60
1 MKAILIPFLSLIPLTPQSAFAQSEPELKLSESVIVSRHGVRAPTKATQMLQMDVTPDAMP 60

Db 61 TWPVKLGELTPRGSELIAVIGHYWRQRLVADGLPKCCGCPQSGQVAIIADVDERTKXGE 120
61 TWPVKLGELTPRGSELIAVIGHYWRQRLVADGLPKCCGCPQSGQVAIIADVDERTKXGE 120

QY 121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180
121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180

Db 121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180
121 APAAGIAPDCAITVHTQADTSSPDLFNPILKTGVCQLDNANVTDAILERAGGSIDPFTGH 180

QY 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

Db 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

QY 241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300
241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300

Db 241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300
241 EIFLLQQAQMPPEGKRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIXTA 300

QY 301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360
301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360

Db 301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360
301 LTPHPPOKAYGVLTPTSVLFIAGHDNTLNLGALBLNMTLPGQPDNTPPGSELVFERW 360

QY 361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420
361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420

Db 361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420
361 RRLSDNSQWISIVFQTLQOMRDKTPLSLNTPGEXYKLTLAGCEERNAQMGSLAGFTQ 420

QY 421 IVNEARIPACSL 432
421 IVNEARIPACSL 432

Db 421 IVNEARIPACSL 432
421 IVNEARIPACSL 432

RESULT 5
US-10-156-660-4
Sequence 4, Application US/10156660
Publication No. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: PHYASERS, NUCLEIC ACIDS ENCODING THEM
AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US/10/156,660
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25

;; PRIOR APPLICATION NUMBER: US 09/291,931
;; PRIOR FILING DATE: 1999-04-13
;; PRIOR APPLICATION NUMBER: US 09/259,214
;; PRIOR FILING DATE: 1999-03-01
;; PRIOR APPLICATION NUMBER: US 08/910,798
;; PRIOR FILING DATE: 1997-08-13
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 432
;; TYPE: PRF
;; ORGANISM: Escherichia coli
US-10-156-660-4

Query Match 96.6%; Score 2182; DB 14; Length 432;
Best Local Similarity 98.1%; Pred. No. 7.6e-201;
Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60
DB 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60
QY 61 TWPVKLGELTPRGELIAYLGHWQRVLVADGLPKCGCPQSGQVAIIADVERTRTKGE 120
DB 61 TWPVKLGELTPRGELIAYLGHWQRVLVADGLPKCGCPQSGQVAIIADVERTRTKGE 120
QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPDKTGVQCLDNNAVTDAILERAGGSIADFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPDKTGVQCLDNNAVTDAILERAGGSIADFTGH 180
QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPDKTGVQCLDNNAVTDAILERAGGSIADFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPDKTGVQCLDNNAVTDAILERAGGSIADFTGH 180
QY 181 YOTAFRELERVLPFQSNLCLKREKODESCSLTQALPELKVSDCVSLTGAVALASMLT 240
DB 181 YOTAFRELERVLPFQSNLCLKREKODESCSLTQALPELKVSDCVSLTGAVALASMLT 240
QY 241 EIFLLQAOAGMPPEKGRITDSHQNNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300
DB 241 EIFLLQAOAGMPPEKGRITDSHQNNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300
QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANLGALELNTLTPGQDNTPPGSELVERW 360
DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANLGALELNTLTPGQDNTPPGSELVERW 360
QY 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCEBNAQMCISLAGFTQ 420
DB 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCEBNAQMCISLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432

RESULT 6
US-09-777-566A-2
;; Sequence 2, Application US/09777566A
;; Patent No. US20010055788A1
;; GENERAL INFORMATION:
;; APPLICANT: DIVERSA CORPORATION
;; APPLICANT: SHORT, Jay
;; APPLICANT: KREITZ, Keith
;; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHRYASES AND USES THEREOF
;; FILE REFERENCE: DIVER1370-6
;; CURRENT APPLICATION NUMBER: US/09/777,566A
;; PRIOR FILING DATE: 2001-06-11
;; PRIOR APPLICATION NUMBER: US 09/318,528
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: US 09/291,931
;; PRIOR FILING DATE: 1999-04-13
;; PRIOR APPLICATION NUMBER: US 09/259,214
;; PRIOR FILING DATE: 1999-03-01
;; PRIOR APPLICATION NUMBER: US 08/910,798
;; PRIOR FILING DATE: 1997-08-13
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.0

;; SEQ ID NO 2
;; LENGTH: 440
;; TYPE: PRF
;; ORGANISM: Escherichia coli
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)-(1323)
;; OTHER INFORMATION: n is any nucleotide
US-09-777-566A-2

Query Match 96.1%; Score 2171; DB 9; Length 440;
Best Local Similarity 97.7%; Pred. No. 8.9e-200;
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60
DB 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60
QY 61 TWPVKLGELTPRGELIAYLGHWQRVLVADGLPKCGCPQSGQVAIIADVERTRTKGE 120
DB 61 TWPVKLGELTPRGELIAYLGHWQRVLVADGLPKCGCPQSGQVAIIADVERTRTKGE 120
QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPDKTGVQCLDNNAVTDAILERAGGSIADFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPDKTGVQCLDNNAVTDAILERAGGSIADFTGH 180
QY 181 YOTAFRELERVLPFQSNLCLKREKODESCSLTQALPELKVSDCVSLTGAVALASMLT 240
DB 181 YOTAFRELERVLPFQSNLCLKREKODESCSLTQALPELKVSDCVSLTGAVALASMLT 240
QY 241 EIFLLQAOAGMPPEKGRITDSHQNNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300
DB 241 EIFLLQAOAGMPPEKGRITDSHQNNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300
QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANLGALELNTLTPGQDNTPPGSELVERW 360
DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANLGALELNTLTPGQDNTPPGSELVERW 360
QY 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCEBNAQMCISLAGFTQ 420
DB 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCEBNAQMCISLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432

RESULT 7
US-09-866-379-2
;; Sequence 2, Application US/09866379
;; Patent No. US20020136754A1
;; GENERAL INFORMATION:
;; APPLICANT: DIVERSA CORPORATION
;; APPLICANT: SHORT, Jay
;; APPLICANT: KREITZ, Keith
;; APPLICANT: GRAY, Kevin
;; APPLICANT: BARTON, Nelson
;; APPLICANT: GARRETT, James
;; APPLICANT: O'DONOGHUE, Eileen
;; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHRYASES AND USES THEREOF
;; FILE REFERENCE: DIVER1370-7
;; CURRENT APPLICATION NUMBER: US/09/866,379
;; PRIOR FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: US 09/580,515
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: US 09/318,528
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: US 09/291,931
;; PRIOR FILING DATE: 1999-04-13
;; PRIOR APPLICATION NUMBER: US 09/259,214
;; PRIOR FILING DATE: 1999-03-01
;; PRIOR APPLICATION NUMBER: US 08/910,798
;; PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.1
SEQ ID NO 2
LENGTH: 440
TYPE: PRT
ORGANISM: Escherichia coli
US-09-866-379-2

Query Match 96.1%; Score 2171; DB 9; Length 440;
Best Local Similarity 97.7%; Pred. No. 8.9e-200;

Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MKAIIIPFSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQIMQDVTDPDAMP 60
DB 1 MKAIIIPFSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQIMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120
DB 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120
QY 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
QY 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
QY 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
QY 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANTGALIELNMTLPGQPDNTPPGGELVFERW 360
DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANTGALIELNMTLPGQPDNTPPGGELVFERW 360
QY 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVKTLLAGCERNNAQMGCSLAGFTQ 420
DB 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVKTLLAGCERNNAQMGCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432
```

RESULT 8

US-10-034-985-2
Sequence 2, Application US/10034985
Publication No. US20030049815A1
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/10/034,985
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
TYPE: PRT
ORGANISM: Escherichia coli
US-10-034-985-2

Query Match 96.1%; Score 2171; DB 14; Length 440;
Best Local Similarity 97.7%; Pred. No. 8.9e-200;

Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
QY 1 MKAIIIPFSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQIMQDVTDPDAMP 60
DB 1 MKAIIIPFSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQIMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120
DB 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120
QY 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
QY 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
DB 121 AFAAGLAPDCAITVHTQADTSSPDLFNPDKTGVCCQDNNANTDAILERAGSIAIDFTGH 180
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
QY 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
QY 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQNTLLSLHNAQFYLLQRTPEVARSATPILLDLIKTA 300
QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANTGALIELNMTLPGQPDNTPPGGELVFERW 360
DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANTGALIELNMTLPGQPDNTPPGGELVFERW 360
QY 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVKTLLAGCERNNAQMGCSLAGFTQ 420
DB 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVKTLLAGCERNNAQMGCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432
```

RESULT 9

US-10-430-356-2
Sequence 2, Application US/10430356
Publication No. US20030232041A1
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/10/430,356
PRIOR FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
TYPE: PRT
ORGANISM: Escherichia coli
US-10-430-356-2

Query Match 96.1%; Score 2171; DB 15; Length 440;
Best Local Similarity 97.7%; Pred. No. 8.9e-200;

Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
QY 1 MKAIIIPFSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQIMQDVTDPDAMP 60
DB 1 MKAIIIPFSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQIMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120
DB 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120
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Db 61 TWPVKGWLTFRGSELAVLGHYORLVDGLLAKKGCPOSGQVAILADVDERTRKGE 120
Qy 121 AFAAGLAPDCATYHTTQADTSSPDPLFNPPLKTCVQCDNANVTALLERAGGSIADTGH 180
Db 121 AFAAGLAPDCATYHTTQADTSSPDPLFNPPLKTCVQCDNANVTALLERAGGSIADTGH 180
Qy 181 YQTAFFRELERVLPFQSNLCKREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
Db 181 RQTAFFRELERVLPFQSNLCKREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
Qy 241 EFLFLQOAGQMPBPWGKRTTDSHOWNTLISLHNAQFDLLQSTPEVARSRAPIPLDLIKTA 300
Db 241 EFLFLQOAGQMPBPWGKRTTDSHOWNTLISLHNAQFDLLQSTPEVARSRAPIPLDLIKTA 300
Qy 301 LTPHPPOKQAVGVTLPSTVLFAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERW 360
Db 301 LTPHPPOKQAVGVTLPSTVLFAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERW 360
Qy 361 RLSDNSQMTQVSLVFQTLQONRDKTPLUSLNTPEGEVKTLAGCEERNAQMGCSLAGFTQ 420
Db 361 RLSDNSQMTQVSLVFQTLQONRDKTPLUSLNTPEGEVKTLAGCEERNAQMGCSLAGFTQ 420
Qy 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432

RESULT 10

US-10-334-672-1
; Sequence 1, Application US/10334672
; Publication No. US20030157646A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; APPLICANT: Koeft, Edward
; TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed
; FILE REFERENCE: SYNG-P01-001
; CURRENT APPLICATION NUMBER: US/10/334,672
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 60/344,523
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030157646A19X Phytase
US-10-334-672-1

Query Match 95.5%; Score 2157; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.8e-198;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 AOSEPELKESVTVSRHGVRAPTKATQLMQDVTDPAMTFVVKGLTPRGSELIAVYG 81
Db 2 AOSEPELKESVTVSRHGVRAPTKATQLMQDVTDPAMTFVVKGLTPRGSELIAVYG 81
Qy 82 HWMRQRLVADGLLPKCGCPQSGQVAILADVDERTRKTEGAPFAAGLAPDCATVHTQADTS 141
Db 82 HWMRQRLVADGLLPKCGCPQSGQVAILADVDERTRKTEGAPFAAGLAPDCATVHTQADTS 141
Qy 142 SPDPLENPPLKTCVQCDNANVTDAIIRAGGSIADFTGHYQTAFFRELERVLPFQSNLCL 201
Db 142 SPDPLENPPLKTCVQCDNANVTDAIIRAGGSIADFTGHYQTAFFRELERVLPFQSNLCL 201
Qy 202 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQOAGMPBPWGKRTD 261
Db 202 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQOAGMPBPWGKRTD 261
Qy 241 IYNEARIPACSL 432
Db 241 IYNEARIPACSL 432

Db 242 SHOWNTLISLHNAQFDLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 301
Qy 322 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQO 381
Db 302 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQO 361
Qy 382 MDKTPSLINTPEGEVKTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 432
Db 362 MDKTPSLINTPEGEVKTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 412

RESULT 11

US-10-334-671-1
; Sequence 1, Application US/10334671
; Publication No. US20030170293A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; APPLICANT: Koeft, Edward
; TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed
; FILE REFERENCE: 70098
; CURRENT APPLICATION NUMBER: US/10/334,671
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 60/344,523
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030170293A19X Phytase
US-10-334-671-1

Query Match 95.5%; Score 2157; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.8e-198;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 AOSEPELKESVTVSRHGVRAPTKATQLMQDVTDPAMTFVVKGLTPRGSELIAVYG 81
Db 2 AOSEPELKESVTVSRHGVRAPTKATQLMQDVTDPAMTFVVKGLTPRGSELIAVYG 81
Qy 82 HWMRQRLVADGLLPKCGCPQSGQVAILADVDERTRKTEGAPFAAGLAPDCATVHTQADTS 141
Db 82 HWMRQRLVADGLLPKCGCPQSGQVAILADVDERTRKTEGAPFAAGLAPDCATVHTQADTS 141
Qy 142 SPDPLENPPLKTCVQCDNANVTDAIIRAGGSIADFTGHYQTAFFRELERVLPFQSNLCL 201
Db 142 SPDPLENPPLKTCVQCDNANVTDAIIRAGGSIADFTGHYQTAFFRELERVLPFQSNLCL 201
Qy 202 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQOAGMPBPWGKRTD 261
Db 202 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQOAGMPBPWGKRTD 261
Qy 262 SHOWNTLISLHNAQFDLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 321
Db 262 SHOWNTLISLHNAQFDLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 301
Qy 322 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQO 381
Db 302 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQO 361
Qy 382 MDKTPSLINTPEGEVKTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 432
Db 362 MDKTPSLINTPEGEVKTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 412

RESULT 12

US-10-021-723A-13
; Sequence 13, Application US/10021723A
; Publication No. US20030101476A1
; GENERAL INFORMATION:

/ APPLICANT: Short, Jay
 / APPLICANT: Mathur, Eric
 / APPLICANT: Richardson, Toby
 / APPLICANT: Robertson, Dan
 / APPLICANT: Barton, Nelson
 / TITLE OF INVENTION: Recombinant Phytases and Uses Thereof
 / FILE REFERENCE: 112766.140 (DIV-016CIP)
 / CURRENT APPLICATION NUMBER: US/10/021.723A
 / CURRENT FILING DATE: 2002-10-23
 / PRIOR APPLICATION NUMBER: US 60/255,090
 / PRIOR FILING DATE: 2000-12-12
 / NUMBER OF SEQ ID NOS: 74
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 13
 / LENGTH: 410
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURES:
 / OTHER INFORMATION: amino acid sequence of a phytase enzyme with
 / OTHER INFORMATION: predicted glycosylation sites
 US-10-021-723A-13

Query Match 95.3%; Score 2153; DB 14; Length 410;
 Best Local Similarity 100.0%; Pred. No. 4.3e-198;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 QSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMPVVKLGELTPRGELIAYIGH 82
 DB 1 QSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMPVVKLGELTPRGELIAYIGH 60
 QY 83 YMRRLVADGGLPKCGCPQSGVAIIADVDERTRKTGEAPAGLAPDCAITVHTQADTSS 142
 DB 61 YMRRLVADGGLPKCGCPQSGVAIIADVDERTRKTGEAPAGLAPDCAITVHTQADTSS 120
 QY 143 PDPLFNPPLKTVGCQLDNNVTDALIERAGSIAFTGHYQTAFFRELERVLPQSNCLK 202
 DB 121 PDPLFNPPLKTVGCQLDNNVTDALIERAGSIAFTGHYQTAFFRELERVLPQSNCLK 180
 QY 203 REKODESGSLTQALPSELKVSADCVSLGAVSLASMLTEIFLLQQAQMPBGMGRITDS 262
 DB 181 REKODESGSLTQALPSELKVSADCVSLGAVSLASMLTEIFLLQQAQMPBGMGRITDS 240
 QY 263 HOWNTLISLHNAQFDLQRTPEVARSRATPLLDLTKALTPEHPPOKAYGVTLPSTVLF 322
 DB 241 HOWNTLISLHNAQFDLQRTPEVARSRATPLLDLTKALTPEHPPOKAYGVTLPSTVLF 300
 QY 323 AGHDTNLANLGGALFLNMTLPGQPDNTPPGELVFERRRRLSDNSQWIOVSLVFQTLQOM 382
 DB 301 AGHDTNLANLGGALFLNMTLPGQPDNTPPGELVFERRRRLSDNSQWIOVSLVFQTLQOM 360
 QY 383 RDKTPLSLNTPPGEVKLTLAGCERNNAQMCSLAGFTQIVNEARIPACSL 432
 DB 361 RDKTPLSLNTPPGEVKLTLAGCERNNAQMCSLAGFTQIVNEARIPACSL 410

RESULT 13
 US-10-021-723A-15
 / Sequence 15, Application US/10021723A
 / Publication No. US20030101476A1
 / GENERAL INFORMATION:
 / APPLICANT: Short, Jay
 / APPLICANT: Mathur, Eric
 / APPLICANT: Richardson, Toby
 / APPLICANT: Robertson, Dan
 / APPLICANT: Barton, Nelson
 / TITLE OF INVENTION: Recombinant Phytases and Uses Thereof
 / FILE REFERENCE: 112766.140 (DIV-016CIP)
 / CURRENT APPLICATION NUMBER: US/10/021.723A
 / CURRENT FILING DATE: 2002-10-23
 / PRIOR APPLICATION NUMBER: US 60/255,090
 / PRIOR FILING DATE: 2000-12-12
 / NUMBER OF SEQ ID NOS: 74
 / SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 15
 / LENGTH: 410
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURES:
 / OTHER INFORMATION: amino acid sequence of a phytase enzyme with
 / OTHER INFORMATION: predicted glycosylation sites
 US-10-021-723A-15

Query Match 95.3%; Score 2153; DB 14; Length 410;
 Best Local Similarity 100.0%; Pred. No. 4.3e-198;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 QSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMPVVKLGELTPRGELIAYIGH 82
 DB 1 QSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMPVVKLGELTPRGELIAYIGH 60
 QY 83 YMRRLVADGGLPKCGCPQSGVAIIADVDERTRKTGEAPAGLAPDCAITVHTQADTSS 142
 DB 61 YMRRLVADGGLPKCGCPQSGVAIIADVDERTRKTGEAPAGLAPDCAITVHTQADTSS 120
 QY 143 PDPLFNPPLKTVGCQLDNNVTDALIERAGSIAFTGHYQTAFFRELERVLPQSNCLK 202
 DB 121 PDPLFNPPLKTVGCQLDNNVTDALIERAGSIAFTGHYQTAFFRELERVLPQSNCLK 180
 QY 203 REKODESGSLTQALPSELKVSADCVSLGAVSLASMLTEIFLLQQAQMPBGMGRITDS 262
 DB 181 REKODESGSLTQALPSELKVSADCVSLGAVSLASMLTEIFLLQQAQMPBGMGRITDS 240
 QY 263 HOWNTLISLHNAQFDLQRTPEVARSRATPLLDLTKALTPEHPPOKAYGVTLPSTVLF 322
 DB 241 HOWNTLISLHNAQFDLQRTPEVARSRATPLLDLTKALTPEHPPOKAYGVTLPSTVLF 300
 QY 323 AGHDTNLANLGGALFLNMTLPGQPDNTPPGELVFERRRRLSDNSQWIOVSLVFQTLQOM 382
 DB 301 AGHDTNLANLGGALFLNMTLPGQPDNTPPGELVFERRRRLSDNSQWIOVSLVFQTLQOM 360
 QY 383 RDKTPLSLNTPPGEVKLTLAGCERNNAQMCSLAGFTQIVNEARIPACSL 432
 DB 361 RDKTPLSLNTPPGEVKLTLAGCERNNAQMCSLAGFTQIVNEARIPACSL 410

RESULT 14
 US-10-284-962-3
 / Sequence 3, Application US/10284962
 / Publication No. US20030206913A1
 / GENERAL INFORMATION:
 / APPLICANT: Webel, Douglas M.
 / APPLICANT: Orr, Donald E.
 / APPLICANT: Rich, Frank E.
 / TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
 / FILE REFERENCE: 834460-71725
 / CURRENT APPLICATION NUMBER: US/10/284,962
 / CURRENT FILING DATE: 2002-10-31
 / PRIOR APPLICATION NUMBER: US 60/335,303
 / PRIOR FILING DATE: 2001-10-31
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 3
 / LENGTH: 432
 / TYPE: PRT
 / ORGANISM: Escherichia coli
 US-10-284-962-3

Query Match 95.1%; Score 2147; DB 15; Length 432;
 Best Local Similarity 96.8%; Pred. No. 1.8e-197;
 Matches 418; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60
 DB 1 MKAILIPFLSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60
 QY 61 TWPVKLGELTPRGELIAYIGHYMRRLVADGGLPKCGCPQSGVAIIADVDERTRKTGE 120

Db 61 TWPKLGMWLPKGGELIAYIGHYORLIVADGLAKGCCQPCQVAILADVDETRKTGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQIDNANVTDAITIERAGSSIAFTGH 180
Db 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQIDNANVTDAITIERAGSSIAFTGH 180
QY 181 YQTAERELERLNPQSNCLIKREKODSCSLTQALSELKVSADCVSLGAVSLASMLT 240
Db 181 RQTAERELERLNPQSNCLIKREKODSCSLTQALSELKVSADCVSLGAVSLASMLT 240
QY 241 EIFLLQQAQGMPEBPGMGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRAATPLIDLIMAA 300
Db 241 EIFLLQQAQGMPEBPGMGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRAATPLIDLIMAA 300
QY 301 LTPHPQQAQAVGTVLPTSVLFIAGHDNTLANLGALBELNMTLPQOPDNTPPGGELVEERW 360
Db 301 LTPHPQQAQAVGTVLPTSVLFIAGHDNTLANLGALBELNMTLPQOPDNTPPGGELVEERW 360
QY 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVCLTLAGEBENNAQCMCSLAGFTQ 420
Db 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVCLTLAGEBENNAQCMCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432

RESULT 15

US-10-284-962-14
; Sequence 14, Application US/10284962
; Publication No. US20030206913A1
; GENERAL INFORMATION:
; APPLICANT: Webel, Douglas M.
; APPLICANT: Orr, Donald E.
; APPLICANT: Ruch, Frank E.
; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
; FILE REFERENCE: 834460-71725
; CURRENT APPLICATION NUMBER: US/10/284,962
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/335,303
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.1
; SEQ ID NO 14
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-284-962-14

Query Match 95.1%; Score 2147; DB 15; Length 432;

Best Local Similarity 96.8%; Pred. No. 1.8e-197;
Matches 418; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLTPQSAFAQSEBELKLSVIVSRHGVRAPTKATQLMQDVTTPDAMP 60
Db 1 MKAILIPFLSLIPLTPQSAFAQSEBELKLSVIVSRHGVRAPTKATQLMQDVTTPDAMP 60
QY 61 TWPVKLGMWLPKGGELIAYIGHYORLIVADGLAKGCCQPCQVAILADVDETRKTGE 120
Db 61 TWPVKLGMWLPKGGELIAYIGHYORLIVADGLAKGCCQPCQVAILADVDETRKTGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQIDNANVTDAITIERAGSSIAFTGH 180
Db 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQIDNANVTDAITIERAGSSIAFTGH 180
QY 181 YQTAERELERLNPQSNCLIKREKODSCSLTQALSELKVSADCVSLTGAVSLASMLT 240
Db 181 RQTAERELERLNPQSNCLIKREKODSCSLTQALSELKVSADCVSLTGAVSLASMLT 240
QY 241 EIFLLQQAQGMPEBPGMGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRAATPLIDLIMAA 300
Db 241 EIFLLQQAQGMPEBPGMGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRAATPLIDLIMAA 300

QY 301 LTPHPQQAQAVGTVLPTSVLFIAGHDNTLANLGALBELNMTLPQOPDNTPPGGELVEERW 360
Db 301 LTPHPQQAQAVGTVLPTSVLFIAGHDNTLANLGALBELNMTLPQOPDNTPPGGELVEERW 360
QY 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVCLTLAGEBENNAQCMCSLAGFTQ 420
Db 361 RLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPPGEVCLTLAGEBENNAQCMCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432

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Job time: 89 secs

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 21:42:28 ; Search time 531.107 Seconds
(without alignments)
1140.289 Million cell updates/sec

Title: US-09-866-379D-9

Perfect score: 1308
Sequence: 1 atgaagcgatctatccc.....gcagttgagatctatcra 1308

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2936184 seqs, 226173202 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1308	100.0	1308	15	US-10-156-660-1 Sequence 1, Appl1
2	1265	96.7	1323	9	US-09-777-566A-1 Sequence 1, Appl1
3	1265	96.7	1323	9	US-09-866-379-1 Sequence 1, Appl1
4	1265	96.7	1323	15	US-10-034-985-1 Sequence 1, Appl1
5	1265	96.7	1323	16	US-10-430-356-1 Sequence 1, Appl1
6	1264	96.6	1299	13	US-10-282-122A-7167 Sequence 7167, Ap
7	1263.8	96.6	1291	9	US-09-866-379-6 Sequence 6, Appl1
8	1263.8	96.6	1291	9	US-09-866-379-7 Sequence 7, Appl1
9	1263.8	96.6	1291	15	US-10-156-660-3 Sequence 3, Appl1
10	1262.2	96.5	1901	9	US-09-866-379-5 Sequence 5, Appl1
11	1262.2	96.5	1901	9	US-09-866-379-9 Sequence 9, Appl1
12	1228	93.9	1489	15	US-10-266-041-9 Sequence 1, Appl1
13	1428	93.9	1489	15	US-10-284-962-1 Sequence 4, Appl1
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22	164.2	12.6	254	16	US-10-317-444-301 Sequence 302, App
23	164.2	12.6	254	16	US-10-317-444-302 Sequence 303, App
24	164.2	12.6	254	16	US-10-317-444-304 Sequence 304, App
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32	35.4	2.7	2781	9	US-09-764-847-1364 Sequence 1364, Ap
33	35.4	2.7	2781	15	US-10-092-154-1364 Sequence 1792, App
34	35.2	2.7	7164	16	US-10-062-674-1792 Sequence 121, App
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45	33.8	2.6	1140	16	US-10-369-493-38716 Sequence 38716, A

ALIGNMENTS

RESULT 1
US-10-156-660-1
Sequence 1, Application US/10156660
Publication NO. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: PHYLASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US/10156,660
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/310,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1308
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified phytase enzyme

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 Sequence 1, Application US/09777566A
 Patent No. US20010055788A1
 GENERAL INFORMATION:
 APPLICANT: DIVERSA CORPORATION
 APPLICANT: SHORT, Jay
 APPLICANT: KRETZ, Keith
 TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
 FILE REFERENCE: DIVERS170-6
 CURRENT APPLICATION NUMBER: US/09/777,566A
 CURRENT FILING DATE: 2001-06-11
 PRIOR APPLICATION NUMBER: US 09/318,528
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: US 09/291,931
 PRIOR FILING DATE: 1999-04-13
 PRIOR APPLICATION NUMBER: US 09/259,214
 PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: US 08/910,798
 PRIOR FILING DATE: 1997-08-13
 NUMBER OF SEQ ID NOS: 4
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 NAME/KEY: CDS
 LOCATION: (1)..(1320)
 NAME/KEY: misc_feature
 LOCATION: (1)..(1323)
 OTHER INFORMATION: n is any nucleotide
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 ; Sequence 1, Application US/09866379
 ; Patent No. US20020136754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: SHORT, Jay
 ; APPLICANT: KREIZ, Keith
 ; APPLICANT: GRAY, Kevin
 ; APPLICANT: BARTON, Nelson
 ; APPLICANT: GARRETT, James
 ; APPLICANT: O'DONOGHUE, Eileen
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHAGES AND USES THEREOF
 ; FILE REFERENCE: DIVER1370-7
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: US 09/580,515
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 09/318,528
 ; PRIOR FILING DATE: 1999-05-25
 ; PRIOR APPLICATION NUMBER: US 09/291,931
 ; PRIOR FILING DATE: 1999-04-13
 ; PRIOR APPLICATION NUMBER: US 09/259,214
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: US 08/910,798
 ; PRIOR FILING DATE: 1997-08-13
 ; NUMBER OF SEQ ID NOS: 10
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 ; SEQ ID NO 1
 ; LENGTH: 1323
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; NAME/KEY: misc feature
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 ; LOCATION: (1)..(1323)
 ; OTHER INFORMATION:
 US-09-866-379-1
 Query Match 96.7%; Score 1265; DB 9; Length 1323;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Qy 1261 ATCGTGAATGAAGCAGCATACCGCGGTGAGTGTGAGATCTCATC 1306
Db 1261 ATCGTGAATGAAGCAGCATACCGCGGTGAGTGTGAGATCTCATC 1306

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RESULT 4
US-10-034-985-1
; Sequence 1, Application US/10034985
; Publication No. US20030049815A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith

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; TITLE OF INVENTION: NOVEL PHYLASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/034,985
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-034-985-1

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Query Match 96.7%; Score 1265; DB 15; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 1 ATGAAAGGATCTTAATCCATTTTATCTCTGATTCGTTAACCAGCAATCTGCA 60
Db 1 ATGAAAGGATCTTAATCCATTTTATCTCTGATTCGTTAACCAGCAATCTGCA 60
Qy 61 TTGCTGAGAGTGAGCCGAGCTGAAGTGAAGTGTGATTTGATGCTGCTAGGT 120
Db 61 TTGCTGAGAGTGAGCCGAGCTGAAGTGAAGTGTGATTTGATGCTGCTAGGT 120
Qy 121 GTGCGTGTCCCAACCAAGGACGACGCACTGATGAGATGCAACCCAGAGCATG 180
Db 121 GTGCGTGTCCCAACCAAGGACGACGCACTGATGAGATGCAACCCAGAGCATG 180
Qy 121 GTGCGTGTCCCAACCAAGGACGACGCACTGATGAGATGCAACCCAGAGCATG 180
Db 121 GTGCGTGTCCCAACCAAGGACGACGCACTGATGAGATGCAACCCAGAGCATG 180
Qy 181 AACTGCGCGGTAAACCTGAGTGAACACGCGCGGTGTGATGCTATGCTC 240
Db 181 AACTGCGCGGTAAACCTGAGTGAACACGCGCGGTGTGATGCTATGCTC 240
Qy 241 GGAATTAATGCGCGTCAAGCTGCTGATGCGGACGATTTGCTTAATGCTGCG 300
Db 241 GGAATTAATGCGCGTCAAGCTGCTGATGCGGACGATTTGCTTAATGCTGCG 300
Qy 301 CAGTGTGTGAGGTGCGATTAATGCTGATGCGAGGCTACCCGTAACAGGCGAA 360
Db 301 CAGTGTGTGAGGTGCGATTAATGCTGATGCGAGGCTACCCGTAACAGGCGAA 360
Qy 361 GCGTTGCGCGCGCGGCTGACCTGACCTGCAATTAACGTAACAGGATGAG 420
Db 361 GCGTTGCGCGCGCGGCTGACCTGACCTGCAATTAACGTAACAGGATGAG 420
Qy 421 TCCAGTCCCGATCCGTTATTATTAATCTCTAATAAACTGGCGTTTCCCACTG 480
Db 421 TCCAGTCCCGATCCGTTATTATTAATCTCTAATAAACTGGCGTTTCCCACTG 480
Qy 481 AACGTGACTGAGCGATCTCTGAGAGGGCGAGAGGTTGCTGACTTTACCGGGCAT 540
Db 481 AACGTGACTGAGCGATCTCTGAGAGGGCGAGAGGTTGCTGACTTTACCGGGCAT 540
Qy 541 TATCAAAACGCGCTTTGCGGAATGGAACGCGGTCTTAATTTTCCGAACTCAACTG 600
Db 541 TATCAAAACGCGCTTTGCGGAATGGAACGCGGTCTTAATTTTCCGAACTCAACTG 600
Qy 601 CTTAAACGTGAGAAACAGACGAAAGCTGTTCACTTAACGAGGATTAACGATGGAATC 660
Db 601 CTTAAACGTGAGAAACAGACGAAAGCTGTTCACTTAACGAGGATTAACGATGGAATC 660

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Qy 661 AAGGTGAGCGCGCACTGTCTCTAATTAACCGGTGCGGTAAAGCTTCGCATCAATGCTGACG 720
Db 661 AAGGTGAGCGCGCACTGTCTCTAATTAACCGGTGCGGTAAAGCTTCGCATCAATGCTGACG 720
Qy 721 GAGATATTTCTCTGCAACAGCAACGAGGAAATGCGAGCGCGGTGGGAGAGATCAC 780
Db 721 GAGATATTTCTCTGCAACAGCAACGAGGAAATGCGAGCGCGGTGGGAGAGATCAC 780
Qy 781 GATTCAACACAGTGAACACCTTGTCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
Db 781 GATTCAACACAGTGAACACCTTGTCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
Qy 841 CGCAGCGCAGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 841 CGCAGCGCAGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Qy 901 TTGACGCGCCATCAACGCAAAACAGGCGTATGCTGATTAACCACTTCAGTGTCTG 960
Db 901 TTGACGCGCCATCAACGCAAAACAGGCGTATGCTGATTAACCACTTCAGTGTCTG 960
Qy 961 TTATATCGCCGACACGATATCTAATCTGCAATCTCGCGCGCGCACTGAGACTCACTGG 1020
Db 961 TTATATCGCCGACACGATATCTAATCTGCAATCTCGCGCGCGCACTGAGACTCACTGG 1020
Qy 1021 ACGGTTCCCGGTCAAGCGCGGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1021 ACGGTTCCCGGTCAAGCGCGGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Qy 1081 CGTGGCGTAAACGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 1081 CGTGGCGTAAACGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy 1141 CAGATGCGTAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Db 1141 CAGATGCGTAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Qy 1201 CTGGCAGATGTAAGAGCGAATGCGAGGCGCATGTGTGTTGCGCAGGTTTACGCA 1260
Db 1201 CTGGCAGATGTAAGAGCGAATGCGAGGCGCATGTGTGTTGCGCAGGTTTACGCA 1260
Qy 1261 ATCGGATGTAAGAGCGAATGCGAGGCGCATGTGTGTTGCGCAGGTTTACGCA 1306
Db 1261 ATCGGATGTAAGAGCGAATGCGAGGCGCATGTGTGTTGCGCAGGTTTACGCA 1306

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RESULT 5

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US-10-430-356-1
; Sequence 1, Application US/10430356
; Publication No. US20030232041A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/430,356
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-430-356-1

Query Match      96.7%; Score 1265; DB 16; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0; Mismatches 26; Indels 0; Gaps 0;
Matches 1280; Conservative 0;

Qy 1 ATGAAAGCATCTTAATCCCATTTTATCTCTTGATTCGTTAACC CGCATCTGCA 60
Db 1 ATGAAAGCATCTTAATCCCATTTTATCTCTTGATTCGTTAACC CGCATCTGCA 60
Qy 61 TTGCTCAAGTGAAGCCGGAAGCTGAAAGTGTGTATGTCAGTGTGATGTT 120
Db 61 TTGCTCAAGTGAAGCCGGAAGCTGAAAGTGTGTATGTCAGTGTGATGTT 120
Qy 121 GTGCGTCTCAACCAAGGCGACGCACTGATGCAAGATGTCAACCCAGCATGCGCA 180
Db 121 GTGCGTCTCAACCAAGGCGACGCACTGATGCAAGATGTCAACCCAGCATGCGCA 180
Qy 181 ACCTGCGCGTAAACTGAGTGAAGCTGACACCGCGGTGTAGACTTAATGCTATGTC 240
Db 181 ACCTGCGCGTAAACTGAGTGAAGCTGACACCGCGGTGTAGACTTAATGCTATGTC 240
Qy 241 GGAATTAATGCGCTCAAGGCTGTGTAGCGGAGGATGCTGCTTAATGTGCTGCGCG 300
Db 241 GGAATTAATGCGCTCAAGGCTGTGTAGCGGAGGATGCTGCTTAATGTGCTGCGCG 300
Qy 301 CAGTGTGTCAGTGTGCGATTAATGCTGATGTGCAAGCGTAACTCCGTTAAACAGGCGAA 360
Db 301 CAGTGTGTCAGTGTGCGATTAATGCTGATGTGCAAGCGTAACTCCGTTAAACAGGCGAA 360
Qy 361 GCTTTGCGCGCGCGGCTGGCACTGACTGTGCAATACCTGATACAGGCAATACG 420
Db 361 GCTTTGCGCGCGCGGCTGGCACTGACTGTGCAATACCTGATACAGGCAATACG 420
Qy 421 TCCAGTCCCGATCCGTTATTTATCTCTTAATAAACTGCGGTTTGCAACTGATTAACGCG 480
Db 421 TCCAGTCCCGATCCGTTATTTATCTCTTAATAAACTGCGGTTTGCAACTGATTAACGCG 480
Qy 481 AACGTATCTGACGCGATCTCTGAGAGGCGAGAGGCTCAATTGCTGACTTTACCGGCGAT 540
Db 481 AACGTATCTGACGCGATCTCTGAGAGGCGAGAGGCTCAATTGCTGACTTTACCGGCGAT 540
Qy 541 TATCAACCGCGGTTTGGCGAATGGAACGGGTGCTTAATTTTCGCAATCAACTGTGTC 600
Db 541 TATCAACCGCGGTTTGGCGAATGGAACGGGTGCTTAATTTTCGCAATCAACTGTGTC 600
Qy 601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCAATTAACGAGGATTAACATGCGAACTTC 660
Db 601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCAATTAACGAGGATTAACATGCGAACTTC 660
Qy 661 AAGGTGAGCGCGCATGCTGTCTCATTAACGCGGTGTAAGGCTGCATCAATGCTGACG 720
Db 661 AAGGTGAGCGCGCATGCTGTCTCATTAACGCGGTGTAAGGCTGCATCAATGCTGACG 720
Qy 721 GAGATATTTCTCTGCAACAGCAACGAGGAAATGCGAGCGCGGTGGGAGAGATCAC 780
Db 721 GAGATATTTCTCTGCAACAGCAACGAGGAAATGCGAGCGCGGTGGGAGAGATCAC 780
Qy 781 GATTCAACACAGTGAACACCTTGTCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
Db 781 GATTCAACACAGTGAACACCTTGTCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
Qy 841 CGCAGCGCAGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 841 CGCAGCGCAGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Qy 901 TTGACGCGCCATCAACGCAAAACAGGCGTATGCTGATTAACCACTTCAGTGTCTG 960

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Db      901 TTACGCCCCATCACCGCAAAACAGCGTATGTGTGACATTACCCACTTCAGTACTG 960
QY      961 TTATCGCCGACACGACTACTAACTCGCAATCTCGCGCGCAGCTGAGCTCAACTG 1020
Db      961 TTATTCGCGGACACGACTACTAACTCGCAATCTCGCGCGCAGCTGAGCTCAACTG 1020
QY      1021 ACCTTCCTCCGCTGACCGGATTAACAGCCCGCCAGGTGTGAAGTGTGTTGAACGCTG 1080
Db      1021 ACCTTCCTCCGCTGACCGGATTAACAGCCCGCCAGGTGTGAAGTGTGTTGAACGCTG 1080
QY      1081 CGTCGCTAAGCAGTAACAGCCAGTGTGATTCAGTTCCTGCTGCTTCCAGACTTACAG 1140
Db      1081 CGTCGCTAAGCAGTAACAGCCAGTGTGATTCAGTTCCTGCTGCTTCCAGACTTACAG 1140
QY      1141 CAGATGCTGATTAACAGCCGCTGTCTTAAATACGCGCCCGGAGAGGTGAACCTGACC 1200
Db      1141 CAGATGCTGATTAACAGCCGCTGTCTTAAATACGCGCCCGGAGAGGTGAACCTGACC 1200
QY      1201 CTGGCAGATGTGAAGAGCAAAATGCGCAGGCGATGTGCTTGGCAGGTTTACGCA 1260
Db      1201 CTGGCAGATGTGAAGAGCAAAATGCGCAGGCGATGTGCTTGGCAGGTTTACGCA 1260
QY      1261 ATCGTGAATGAAGCAGCATACCGCGCTGCAATTGAGATCTCATC 1306
Db      1261 ATCGTGAATGAAGCAGCATACCGCGCTGCAATTGAGATCTCATC 1306

RESULT 6
US-10-282-122A-7167
; Sequence 7167, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Fotsych, R.
; APPLICANT: Xu, H.
; FILE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EPIRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7167

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; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-7167
Query Match          96.6%; Score 1264; DB 13; Length 1299;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY      1 ATGAAGGAGCTTTAATCCATTTTATCTCTTGTGATTCGGTTAAACCCGGCAATCGCA 60
Db      1 ATGAAGGAGCTTTAATCCATTTTATCTCTTGTGATTCGGTTAAACCCGGCAATCGCA 60
QY      61 TTCGCTCAGATGAGCCGAGAGCTGAAGTGTGATTTGTCAGTGTGATGAT 120
Db      61 TTCGCTCAGATGAGCCGAGAGCTGAAGTGTGATTTGTCAGTGTGATGAT 120
QY      121 GTGCGTGTCCACCAAGGCGACGCAACTGATGAGATGTCACTCCAGAGCATGAGCCA 180
Db      121 GTGCGTGTCCACCAAGGCGACGCAACTGATGAGATGTCACTCCAGAGCATGAGCCA 180
QY      181 ACCTGCGCGGTAAACTGGGTGAGCTGACACCGCGGTGGTGAATTCGCTATCTC 240
Db      181 ACCTGCGCGGTAAACTGGGTGAGCTGACACCGCGGTGGTGAATTCGCTATCTC 240
QY      241 GGCATTTA CTGGCGGTGACGCTGTGTGTAAGCCGAGATTTGCTGCTTAAATGTGCTGCCG 300
Db      241 GGCATTTA CTGGCGGTGACGCTGTGTGTAAGCCGAGATTTGCTGCTTAAATGTGCTGCCG 300
QY      301 CAGTGTGTGACGTGCGGATTTATGCTGATGTGACGAGGTGATCCGTTAAACAGGCGAA 360
Db      301 CAGTGTGTGACGTGCGGATTTATGCTGATGTGACGAGGTGATCCGTTAAACAGGCGAA 360
QY      361 GCGTTGCGCGCGCGGCTGCGACCTGACTGTGCAATTAACCGTATACCGAGCAGATACG 420
Db      361 GCGTTGCGCGCGCGGCTGCGACCTGACTGTGCAATTAACCGTATACCGAGCAGATACG 420
QY      421 TCGAGTCCCGATCCGTTTATTAATCTCTTAAACTGCGGCTTGGCCAACTGGAATTAAGCG 480
Db      421 TCGAGTCCCGATCCGTTTATTAATCTCTTAAACTGCGGCTTGGCCAACTGGAATTAAGCG 480
QY      481 AACGTGCTGACGCGATCTCGAAGAGGACAGAGGATCAATTTGCTGACTTACCGGCGAT 540
Db      481 AACGTGCTGACGCGATCTCGAAGAGGACAGAGGATCAATTTGCTGACTTACCGGCGAT 540
QY      541 TATCAAACTGCGGTTTCGGAATCTGGAACGGGTCTTAATTTCCGCAATCAACTGTGCG 600
Db      541 TATCAAACTGCGGTTTCGGAATCTGGAACGGGTCTTAATTTCCGCAATCAACTGTGCG 600
QY      601 CTTAAACGTGAAGAACAGAGAGAGCTGTTCAATTAACGACGATTAACATCGGAATC 660
Db      601 CTTAAACGTGAAGAACAGAGAGAGCTGTTCAATTAACGACGATTAACATCGGAATC 660
QY      661 AAGGTGACGCGCGATGTGTCTAATTAACGGTGTGTAAGCTTCGCAATCAATCTGACG 720
Db      661 AAGGTGACGCGCGATGTGTCTAATTAACGGTGTGTAAGCTTCGCAATCAATCTGACG 720
QY      721 GAGATATTCTCTGCAACAGCAAGGAATGCGGAGCCGCGGTGGGGAAGATCAAC 780
Db      721 GAGATATTCTCTGCAACAGCAAGGAATGCGGAGCCGCGGTGGGGAAGATCAAC 780
QY      781 GATTCACACAGTGAACAACCTTGCTAAGTTGCAATACGCGCAATTTGATTGCTACAA 840
Db      781 GATTCACACAGTGAACAACCTTGCTAAGTTGCAATACGCGCAATTTGATTGCTACAA 840
QY      841 CGCAGCGCAGAGGTTCGCGGAGCGCGCGCACCCCGTTATTAATTTGATTAAGACAGCG 900
Db      841 CGCAGCGCAGAGGTTCGCGGAGCGCGCGCACCCCGTTATTAATTTGATTAAGACAGCG 900
QY      901 TTGACGCCCCATCACCGCAAAACAGCGGTATGTGATTAACCATTCAGTGTG 960
Db      901 TTGACGCCCCATCACCGCAAAACAGCGGTATGTGATTAACCATTCAGTGTG 960

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Qy 961 TTATACCGGACACGATCTACTAATCTGCAATCTCGCGCGCACTGAGCTCACTG 1020
Db 961 TTATACCGGACACGATCTACTAATCTGCAATCTCGCGCGCGCACTGAGCTCACTG 1020
Qy 1021 ACGCTTCCCGGTACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAGCTG 1080
Db 1021 ACGCTTCCCGGTACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAGCTG 1080
Qy 1081 CGTGGCGATGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1140
Db 1081 CGTGGCGATGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1140
Qy 1141 CAGATGCGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1200
Db 1141 CAGATGCGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1200
Qy 1201 CTGGCAGATGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1260
Db 1201 CTGGCAGATGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1260
Qy 1261 ATCGTAATGAAGCAGCATACCGCGCTGCACTTTG 1296
Db 1261 ATCGTAATGAAGCAGCATACCGCGCTGCACTTTG 1296

RESULT 7
US-09-866-379-6
Sequence 6, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION.
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHRYASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1901)
OTHER INFORMATION: n is any nucleotide
US-09-866-379-6

Query Match 96.6%; Score 1263.8; DB 9; Length 1901;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 AAGAAAGCAATCTTATCCATTTTATCTCTTCGATTCGCTAACCCCGCAATCTCA 60
Db 188 AAGAAAGCAATCTTATCCATTTTATCTCTTCGATTCGCTAACCCCGCAATCTCA 247
Qy 61 TTCGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTAAGTGTGTAAGCTGATG 120

Db 248 TTCGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTAAGTGTGTAAGCTGATG 307
Qy 121 GTGCGTGTCCAACCAAGGCGACGCACTGATGCAAGTGTCACTCCAGACGATGCGCA 180
Db 308 GTGCGTGTCCAACCAAGGCGACGCACTGATGCAAGTGTCACTCCAGACGATGCGCA 367
Qy 181 ACGTGGCGGATTAACCTGGGTGAGCTGAACCGCGCGGTGTGTAAGTGTGTAAGCT 240
Db 368 ACGTGGCGGATTAACCTGGGTGAGCTGAACCGCGCGGTGTGTAAGTGTGTAAGCT 427
Qy 241 GGAATTAATGAGCGTCTGATGAGCGATGATGATGCTGATTAATGATGATGATG 300
Db 428 GGAATTAATGAGCGTCTGATGAGCGATGATGATGCTGATTAATGATGATGATG 487
Qy 301 CAGTGTGTGAGTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 488 CAGTGTGTGAGTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATG 547
Qy 361 GCTTGGCGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 548 GCTTGGCGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 607
Qy 421 TCCAGTCCCGATCCGTTATTAATCTCTTAAACTGCGCTTTGCCAATGATGATG 480
Db 608 TCCAGTCCCGATCCGTTATTAATCTCTTAAACTGCGCTTTGCCAATGATGATG 667
Qy 481 AAGTGAATGAGCGGATCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 668 AAGTGAATGAGCGGATCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727
Qy 541 TATCAACGCGCTTTGCGCACTGAAACGCGTCTTAATTTTCCGCAATGAACTTGTG 600
Db 728 CGGCAACGCGCTTTGCGCACTGAAACGCGTCTTAATTTTCCGCAATGAACTTGTG 787
Qy 601 CTTAACGATGAAGAAACAGACGAAAGCTGTCTTAACGCAAGCACTTCACTGAACTG 660
Db 788 CTTAACGATGAAGAAACAGACGAAAGCTGTCTTAACGCAAGCACTTCACTGAACTG 847
Qy 661 AAGTGAAGCGCGATGCTCTCACTTAACGCGTGTGAGTGAAGCTGATCAATGCTGAG 720
Db 848 AAGTGAAGCGCGATGCTCTCACTTAACGCGTGTGAGTGAAGCTGATCAATGCTGAG 907
Qy 721 GAGATATTTCTCTGCAACAGCAAGGATGCGGAGCGGAGCGGAGGAGGAGGATGAC 780
Db 908 GAGATATTTCTCTGCAACAGCAAGGATGCGGAGCGGAGCGGAGGAGGAGGATGAC 967
Qy 781 GATTCAACAGGAGAAACCTGTGATGATGATGATGATGATGATGATGATGATGATG 840
Db 968 GATTCAACAGGAGAAACCTGTGATGATGATGATGATGATGATGATGATGATGATG 1027
Qy 841 CGCAAGCGCAGAGGTTCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1028 CGCAAGCGCAGAGGTTCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1087
Qy 901 TTGAAGCGCCATCAACCGCAAAACAGCGGTATGATGATGATGATGATGATGATGATG 960
Db 1088 TTGAAGCGCCATCAACCGCAAAACAGCGGTATGATGATGATGATGATGATGATGATG 1147
Qy 961 TTATGCGCGGACACGATCTATTAATCTGCAATCTGCGCGGCGCATGAGCTCACTG 1020
Db 1148 TTATGCGCGGACACGATCTATTAATCTGCAATCTGCGCGGCGCATGAGCTCACTG 1207
Qy 1021 ACGCTTCCCGGTACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAGCTG 1080
Db 1208 ACGCTTCCCGGTACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAGCTG 1267
Qy 1081 CGTGGCGATGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1140
Db 1268 CGTGGCGATGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAG 1327
Qy 1141 CAGATGCGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAGCTG 1200
Db 1328 CAGATGCGATTAACACGCGGATTAACACGCGCGGAGTGTGTAAGTGTGTAAGCTG 1387

QY 1201 CTGGCAGAGATGTGTAAGAGCGAAATGCCAGAGCATGTGTTCTGGCAGAGTTTACGAA 1260
DB 1388 CTGGCAGAGATGTGTAAGAGCGAAATGCCAGAGCATGTGTTCTGGCAGAGTTTACGAA 1447
QY 1261 ATCGTGAATGAGACGACATACCGCGCTGACAGTTTGAGAT 1300
DB 1448 ATCGTGAATGAGACGACATACCGCGCTGACAGTTTGAT 1487

RESULT 8
US-09-866-379-7

Sequence 7, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHOSPHATASES AND USES THEREOF
FILE REFERENCE: DIVER370-7
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1901)
OTHER INFORMATION: n is any nucleotide
US-09-866-379-7

Query Match 96.6%; Score 1263.8; DB 9; Length 1901;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 ATGAAAGCATCTTATATCCATTTTATCTTTGATTCCTGTTAACCCCGCATCTGCA 60
DB 188 ATGAAAGCATCTTATATCCATTTTATCTTTGATTCCTGTTAACCCCGCATCTGCA 247
QY 61 TTGCGTCAGAGTAGAGCCGAGCTGAAGTGAAGTGTGATTTGTCAGTCTCATGAT 120
DB 248 TTGCGTCAGAGTAGAGCCGAGCTGAAGTGAAGTGTGATTTGTCAGTCTCATGAT 307
QY 121 GTGCGTCTCCAAACCAAGCCACGCACTGATGACGATGTCACCCAGACGATGGCA 180
DB 308 GTGCGTCTCCAAACCAAGCCACGCACTGATGACGATGTCACCCAGACGATGGCA 367
QY 181 ACCTGCGCGGTAAACCTGAGTGAAGTGAAGTGTGATTTGTCAGTCTCATGAT 240
DB 368 ACCTGCGCGGTAAACCTGAGTGAAGTGAAGTGTGATTTGTCAGTCTCATGAT 427
QY 241 GGACATTAATGCGGTGAGTGTGATGACGACGATTTGCTCTAAATGTGCTGCGCG 300
DB 428 GGACATTAATGCGGTGAGTGTGATGACGACGATTTGCTCTAAATGTGCTGCGCG 487
QY 301 CAGTGTGATGAGCAAGCAATACCGCGGTGATTTGAT 1487

DB 488 CAGTGTGATGAGCAAGCAATACCGCGGTGATTTGAT 1487
QY 361 GCCTTCGCGCGCGCTGAGCACTGATGTCATTAACCGTACATACCCAGGAGATACG 420
DB 548 GCCTTCGCGCGCGCTGAGCACTGATGTCATTAACCGTACATACCCAGGAGATACG 607
QY 421 TCCAGTCCCGATTCGCTTATTTATCTCTAAATACTGCGCTTTCGCACTGATTAACGCG 480
DB 608 TCCAGTCCCGATTCGCTTATTTATCTCTAAATACTGCGCTTTCGCACTGATTAACGCG 667
QY 481 AACGTGACTGACGCGATCTTGAAGAGGAGGTCATTTGCTGACTTTAACCGGCGAT 540
DB 668 AACGTGACTGACGCGATCTTGAAGAGGAGGTCATTTGCTGACTTTAACCGGCGAT 727
QY 541 TATCAACGCGGCTTCGGAATGGAACGCGGTGCTTATTTTCGCAATCAACTGTGCG 600
DB 728 CCGCAAAACGCGCTTTCGGAATGGAACGCGGTGCTTATTTTCGCAATCAACTGTGCG 787
QY 601 CTTAAACGTGAGAAACAGAGCAAGAACTGTCATTTAACGAGCATTAACCATTCGAACTC 660
DB 788 CTTAAACGTGAGAAACAGAGCAAGAACTGTCATTTAACGAGCATTAACCATTCGAACTC 847
QY 661 AAGTGAGCGCGCGATGTCATTTAACGAGGTGAGTACCTGCAATCAATGCTGACG 720
DB 848 AAGTGAGCGCGCGATGTCATTTAACGAGGTGAGTACCTGCAATCAATGCTGACG 907
QY 721 GAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGCGGTGAGGAGATCAC 780
DB 908 GAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGCGGTGAGGAGATCAC 967
QY 781 GATTACACCGATGAGAAACCTGCTAGTTGATTAACGAGCATTTGATTTGCTCA 840
DB 968 GATTACACCGATGAGAAACCTGCTAGTTGATTAACGAGCATTTGATTTGCTCA 1027
QY 841 CCGACGCGAGAGTGTGCGCGAGCGCGCAACCCGTTATTAATTGATCAAGACGCG 900
DB 1028 CCGACGCGAGAGTGTGCGCGAGCGCGCAACCCGTTATTAATTGATCAAGACGCG 1087
QY 901 TTGAGCGCCCATCCACCGCAAAACAGGCGTATGATGATTAACCATTCGATGCTG 960
DB 1088 TTGAGCGCCCATCCACCGCAAAACAGGCGTATGATGATTAACCATTCGATGCTG 1147
QY 961 TTATGCGCGGACAGATTAATCTGCAATCTGCGCGCGCACTGAGTCAACTGCG 1020
DB 1148 TTATGCGCGGACAGATTAATCTGCAATCTGCGCGCGCACTGAGTCAACTGCG 1207
QY 1021 AGCGTTCGCGTCAAGCGGATTAACGCGCGCGCACTGAGTCAACTGCG 1080
DB 1208 AGCGTTCGCGTCAAGCGGATTAACGCGCGCGCACTGAGTCAACTGCG 1267
QY 1081 CGTGGCTAAGCGATTAACGCGCGGATTAACGCGCGCGCACTGAGTCAACTGCG 1140
DB 1268 CGTGGCTAAGCGATTAACGCGCGGATTAACGCGCGCGCACTGAGTCAACTGCG 1327
QY 1141 CAGATCGGTATTAACGCGCGGATTAACGCGCGCGCACTGAGTCAACTGCG 1200
DB 1328 CAGATCGGTATTAACGCGCGGATTAACGCGCGCGCACTGAGTCAACTGCG 1387
QY 1201 CTGGCAGAGATGTGTAAGAGCGAAATGCCAGAGCATGTGTTCTGGCAGAGTTTACGAA 1260
DB 1388 CTGGCAGAGATGTGTAAGAGCGAAATGCCAGAGCATGTGTTCTGGCAGAGTTTACGAA 1447
QY 1261 ATCGTGAATGAGACGACATACCGCGCTGACAGTTTGAGAT 1300
DB 1448 ATCGTGAATGAGACGACATACCGCGCTGACAGTTTGAT 1487

RESULT 9
US-10-156-660-3
Sequence 3, Application US/10156660
Publication No. US20030103958A1
GENERAL INFORMATION:

APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Eileen
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 0910-029007
CURRENT APPLICATION NUMBER: US/10/156,660
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
FEATURE:
NAME/KEY: misc feature
LOCATION: 403
OTHER INFORMATION: n = A,T,C or G
US-10-156-660-3

Query Match 96.6%; Score 1263.8; DB 15; Length 1901;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

1 ATGAAGCGATCTTAATCCATTCTTCTGATTCGGTTAACCCGCAATCGCA 60
188 ATGAAGCGATCTTAATCCATTCTTCTGATTCGGTTAACCCGCAATCGCA 247
61 TTCCTCAGAGTGAAGCCGAGCTGAAGCTGAAGAGTGTGATTTGTCATGAT 120
248 TTCCTCAGAGTGAAGCCGAGCTGAAGCTGAAGAGTGTGATTTGTCATGAT 307
121 GTGGGTGCTCAACCAAGGCGCAAGCACTGATGAGATGTCAACCCAGACGATG 180
308 GTGGGTGCTCAACCAAGGCGCAAGCACTGATGAGATGTCAACCCAGACGATG 367
181 ACCTGGCGGTAAGCACTGGGTGAGCTGACACCGCGCGGTGTGAGCTAATCG 240
368 ACCTGGCGGTAAGCACTGGGTGAGCTGACACCGCGCGGTGTGAGCTAATCG 427
241 GGAGATTACTGGCGGTGAGCTGATGAGCGAGATTGCTGCTTAATGATGCGT 300
428 GGAGATTACTGGCGGTGAGCTGATGAGCGAGATTGCTGCTTAATGATGCGT 487
301 CAGTCTGTCAGGTGCGGATTAATGCTGATGTCAGCGAGCGTACCCGTAAAC 360
488 CAGTCTGTCAGGTGCGGATTAATGCTGATGTCAGCGAGCGTACCCGTAAAC 547
361 GCCTTCGCGCGCGGTGCGGATTAATGCTGATGTCAGCGAGCGTACCCGTAA 420
548 GCCTTCGCGCGCGGTGCGGATTAATGCTGATGTCAGCGAGCGTACCCGTAA 607
421 TCAGTCCCGATCCGTTATTAATCTCTTAATAAATGGCGTTTGCACATGATAC 480

608 TCAGTCCCGATCCGTTATTAATCTCTTAATAAATGGCGTTTGCACATGATAC 667
481 AACGTACTGACGCGATCTCGAGAGGCGAGAGGGTCAATTTGCTTAACCGGG 540
668 AACGTACTGACGCGATCTCGAGAGGCGAGAGGGTCAATTTGCTTAACCGGG 727
541 TATCAAGCGCGTTTCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAA 600
728 CGCGAAACGCGCGTTTCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAA 787
601 CTTAACGCGGAAACAGAGAGGAGCGTTTCAATTAAGCGAGGCAATTCATCG 660
788 CTTAACGCGGAAACAGAGAGGAGCGTTTCAATTAAGCGAGGCAATTCATCG 847
661 AAGGTAGCGCGGATCTGCTCATTTAACCGGTGCGTAACTTCGATCAATGTA 720
848 AAGGTAGCGCGGATCTGCTCATTTAACCGGTGCGTAACTTCGATCAATGTA 907
721 GAGATTTTCTCTGCAACAGCAAGGGAATGCGGAGCGGGTGGGGAAGATCA 780
908 GAGATTTTCTCTGCAACAGCAAGGGAATGCGGAGCGGGTGGGGAAGATCA 967
781 GATTCAACAGGTGGAACACTTGTAACTTGAATGCAACGCGCAATTTGATTT 840
968 GATTCAACAGGTGGAACACTTGTAACTTGAATGCAACGCGCAATTTGATTT 1027
841 CGAGCGCCAGAGTTGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
1028 CGAGCGCCAGAGTTGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1087
901 TTGAGCGCCCATCCACCGCAAAAACAGCGGTATGATGATTAACCACTTCA 960
1088 TTGAGCGCCCATCCACCGCAAAAACAGCGGTATGATGATTAACCACTTCA 1147
961 TTTATGCGCGGACAGATTAATCTGCAAAATCTGCGCGGCGCACTGAGCTCA 1020
1148 TTTATGCGCGGACAGATTAATCTGCAAAATCTGCGCGGCGCACTGAGCTCA 1207
1021 ACGCTTCCCGGTCAAGCGGATTAACAGCGCGGCGGAGTGAATCTGTTGA 1080
1208 ACGCTTCCCGGTCAAGCGGATTAACAGCGCGGCGGAGTGAATCTGTTGA 1267
1081 CGTGGCTTAAGGATTAACAGCGGATTAACAGCGGCTTGTGCTTCAACTT 1140
1268 CGTGGCTTAAGGATTAACAGCGGATTAACAGCGGCTTGTGCTTCAACTT 1327
1141 CAGATGCGGATTAACAGCGGATTAACAGCGGCTTGTGCTTCAACTT 1200
1328 CAGATGCGGATTAACAGCGGATTAACAGCGGCTTGTGCTTCAACTT 1387
1201 CTGGCAGATGTAAGAGGGAATGCGAGGATGTTGTTGTTGCAAGTTTAC 1260
1388 CTGGCAGATGTAAGAGGGAATGCGAGGATGTTGTTGTTGCAAGTTTAC 1447
1261 ATCGTGAATGAAGCAAGCAATACCGCGGTGCACTTTGAAT 1300
1448 ATCGTGAATGAAGCAAGCAATACCGCGGTGCACTTTGAAT 1487

RESULT 10
US-09-866-379-5
Sequence 5, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7

Tue May 4 07:05:31 2004

us-09-866-379d-9.rmp

Page 10

CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1901)
OTHER INFORMATION: n is any nucleotide
US-09-866-379-5

Query Match 96.5%; Score 1262.2; DB 9; Length 1901;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGAAAGGATCTTATATCCATTTTATCTCTGATTCGGTTAACCCGCAATTCGCA 60
DB 188 ATGAAAGGATCTTATATCCATTTTATCTCTGATTCGGTTAACCCGCAATTCGCA 247
QY 61 TTGCGTCAGAGTGGCCGAGCTGAAGCTGAAAGTGTGATTTGTCAGTCCGATGGT 120
DB 248 TTGCGTCAGAGTGGCCGAGCTGAAGCTGAAAGTGTGATTTGTCAGTCCGATGGT 307
QY 121 GTGCGTGTCCAAACCAAGGCCACGCACTGATGACAGATGTACCCCAAGACGACGCA 180
DB 308 GTGCGTGTCCAAACCAAGGCCACGCACTGATGACAGATGTACCCCAAGACGACGCA 367
QY 181 ACCTGCGCGGTAAATCTGGTGAAGTGAACCGCGCGGTGTGAGTAAATGCTTATCTC 240
DB 368 ACCTGCGCGGTAAATCTGGTGAAGTGAACCGCGCGGTGTGAGTAAATGCTTATCTC 427
QY 241 GGACATTAATGCGCTGACGCTGTGATACCGACGATTCGCTTAAATGTGCTGCGCG 300
DB 428 GGACATTAACCAACGCGCAAGCTGTGATACCGACGATTCGCTTAAATGTGCTGCGCG 487
QY 301 CAGTCTGTGCTGAGTGGCGATTAATGCTATGTCAACGAGGCTAACCCGTTAAACGCGGAA 360
DB 488 CAGTCTGTGCTGAGTGGCGATTAATGCTATGTCAACGAGGCTAACCCGTTAAACGCGGAA 547
QY 361 GCGTTCGCGCGCGGCGTGGCACTGATGTCATTAACCGTACATACCCAGGACGATACG 420
DB 548 GCGTTCGCGCGCGGCGTGGCACTGATGTCATTAACCGTACATACCCAGGACGATACG 607
QY 421 TCGAGTCCCGATCCGTTATTTATCTCTTAAATACTGCGCTTTGCGCACTGGATTAACGG 480
DB 608 TCGAGTCCCGATCCGTTATTTATCTCTTAAATACTGCGCTTTGCGCACTGGATTAACGG 667
QY 481 AACGTGACTGACGCGATCTCGACAGGCGACGAGGCGCAATTTGCTGATTAACGCGGAT 540
DB 668 AACGTGACTGACGCGATCTCGACAGGCGACGAGGCGCAATTTGCTGATTAACGCGGAT 727
QY 541 TATCAAAAGCGGCTTTGCGCACTGGAACGCGGTGCTTAATTTTCCGCAATCAACTGTGCG 600
DB 728 CGGCAAAAGCGGCTTTGCGCACTGGAACGCGGTGCTTAATTTTCCGCAATCAACTGTGCG 787
QY 601 CTTAAACGTGAGAAACAGGACGAAGCTGTTCATTAACGACGAGCATTAACCATCGGAATC 660
DB 788 CTTAAACGTGAGAAACAGGACGAAGCTGTTCATTAACGACGAGCATTAACCATCGGAATC 847
QY 661 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAAGCTTCGCAATCAATGCTGACG 720

DB 848 AAGGTGAGCGCCGACMAATGTCTCATTAACCGGTGCGGTAAAGCTTCGCAATCAATGCTGACG 907
QY 721 GAGATATTTCTCTCTCAACAAGCACAGGGAATGCGAGCGGAGTGGGGAAGATCAAC 780
DB 908 GAGATATTTCTCTCTCTCAACAAGCACAGGGAATGCGAGCGGAGTGGGGAAGATCAAC 967
QY 781 GATTACACCAAGTGAACCACTTGTCTTAAGTTTGCATTAACGCGCAATTTGATTTGCTACAA 840
DB 968 GATTACACCAAGTGAACCACTTGTCTTAAGTTTGCATTAACGCGCAATTTGATTTGCTACAA 1027
QY 841 CGCAGCGCAGAGTGGCCGCGAGCGCGCAACCCGTTATTAATTTGATCAAGACAGCG 900
DB 1028 CGCAGCGCAGAGTGGCCGCGAGCGCGCAACCCGTTATTAATTTGATCAAGACAGCG 1087
QY 901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGATGACATTAACCACTTCAGTCTG 960
DB 1088 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGATGACATTAACCACTTCAGTCTG 1147
QY 961 TTATGCGCGGACAGATTAATCTGCAATCTCGCGGCGGACCTGAGGCTCACTG 1020
DB 1148 TTATGCGCGGACAGATTAATCTGCAATCTCGCGGCGGACCTGAGGCTCACTG 1207
QY 1021 ACGCTTCCCGGTCAACCGGATTAACAGCGCGCGCAAGTGTGAACCTGTGTTGAACGCTG 1080
DB 1208 ACGCTTCCCGGTCAACCGGATTAACAGCGCGCGCAAGTGTGAACCTGTGTTGAACGCTG 1267
QY 1081 CTTGCGCTAAGGATTAACAGCGAGTGAATTCAGTTTGGCTGCTTCCAGCTTACAG 1140
DB 1268 CTTGCGCTAAGGATTAACAGCGAGTGAATTCAGTTTGGCTGCTTCCAGCTTACAG 1327
QY 1141 CAGATGCTGATTAACAGCGCGCTGTCTTAAATACCGCGCGCGAGAGTGAACCTGAC 1200
DB 1328 CAGATGCTGATTAACAGCGCGCTGTCTTAAATACCGCGCGCGAGAGTGAACCTGAC 1387
QY 1201 CTGGCAGATGTTGAAGAGCGAAATGCGAGGCGCATGTGTTGTTGAGTTTACGGA 1260
DB 1388 CTGGCAGATGTTGAAGAGCGAAATGCGAGGCGCATGTGTTGTTGAGTTTACGGA 1447
QY 1261 ATGCTGATGAAGACGACATACCGGCTGCACTTGAAT 1300
DB 1448 ATGCTGATGAAGACGACATACCGGCTGCACTTGAAT 1487
RESULT 11
US-09-866-379-9
Sequence 9, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KREIZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9

LENGTH: 1901
 TYPE: DNA
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)-(1901)
 OTHER INFORMATION: n is any nucleotide
 US-09-866-379-9

Query Match 96.5%; Score 1262.2; DB 9; Length 1901;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 1276; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

1 ATGAAAGCATCTTAATCCATTTTATCTCTCTGATCCGTTAACCCCGCAATCTGCA 60
 188 ATGAAAGCATCTTAATCCATTTTATCTCTCTGATCCGTTAACCCCGCAATCTGCA 247
 61 TTGCTCAGAGTAGCCCGAGCTGAAAGTGTGTGATTTGTCACTGCTCATGTGT 120
 248 TTGCTCAGAGTAGCCCGAGCTGAAAGTGTGTGATTTGTCACTGCTCATGTGT 307
 121 GTGCTGCTCCAAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCCA 180
 308 GTGCTGCTCCAAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCCA 367
 181 ACCGTGCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTGCTATCTC 240
 368 ACCGTGCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTGCTATCTC 427
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 428 GGAATTAATCTGAGCTCAGCTGTGTGAGCCGACGATTTGCTCTAAATGTGTGCTCC 487
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 361 GCTTTCGCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTGCTATCTC 420
 548 GCTTTCGCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTGCTATCTC 607
 421 TCCAGTGTGCTGAGCTCAGCTGTGTGAGCCGACGATTTGCTCTAAATGTGTGCTCC 480
 608 TCCAGTGTGCTGAGCTCAGCTGTGTGAGCCGACGATTTGCTCTAAATGTGTGCTCC 667
 481 AACGTGCTGAGCTCAGCTGTGTGAGCCGACGATTTGCTCTAAATGTGTGCTCC 540
 668 AACGTGCTGAGCTCAGCTGTGTGAGCCGACGATTTGCTCTAAATGTGTGCTCC 727
 541 TATCAAAAGCGGTTCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 600
 728 CGGCAAAAGCGGTTCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 787
 601 CTAAAGCGGTTCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 660
 788 CTAAAGCGGTTCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 847
 661 AAGGTGAGCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 720
 848 AAGGTGAGCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 907
 721 GAGATATTTCTCTGCAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCC 780
 908 GAGATATTTCTCTGCAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCC 967
 781 GATTCAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCC 840
 968 GATTCAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCC 1027
 841 CGCAAGCGAGAGTTCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 900
 1028 CGCAAGCGAGAGTTCGCGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTG 1087

901 TTGACGCCCATCCACCGCAAAAACAGCGGTATGATGATTAATCCCATTCAGTCTG 960
 1088 TTGACGCCCATCCACCGCAAAAACAGCGGTATGATGATTAATCCCATTCAGTCTG 1147
 961 TTTATGCGCGGACACGATTAATCTGCGCAATCTCGCGCGCGACATGAGCTCACTGG 1020
 1148 TTTATGCGCGGACACGATTAATCTGCGCAATCTCGCGCGCGACATGAGCTCACTGG 1207
 1021 ACGCTTCCCGGTACCGGATTAACACCGCGCGAGTGTGAACTGTGTGAAAGCTGG 1080
 1208 ACGCTTCCCGGTACCGGATTAACACCGCGCGAGTGTGAACTGTGTGAAAGCTGG 1267
 1081 CGTGCCTTAAGGATTAACACCGCGCGAGTGTGAACTGTGTGAAAGCTGG 1140
 1268 CGTGCCTTAAGGATTAACACCGCGCGAGTGTGAACTGTGTGAAAGCTGG 1327
 1141 CAGATGCGGTAAACACCGCGCGAGTGTGAACTGTGTGAAAGCTGG 1200
 1328 CAGATGCGGTAAACACCGCGCGAGTGTGAACTGTGTGAAAGCTGG 1387
 1201 CTGCGAGATGTAAGACGGAATGCGAGGCGATGTGTGCGTTGGCAGTTTAAACGCA 1260
 1388 CTGCGAGATGTAAGACGGAATGCGAGGCGATGTGTGCGTTGGCAGTTTAAACGCA 1447
 1261 ATCGTGAATGAACGCAATACCGCGCGTGTGAGTGTGAGAT 1300
 1448 ATCGTGAATGAACGCAATACCGCGCGTGTGAGTGTGAGAT 1487

RESULT 12

US-10-266-041-9
 ; Sequence 9, Application US/10266041
 ; Publication No. US2003007284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lei, Xinggen
 ; TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
 ; FILE REFERENCE: 19603/2791
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: US/09/540,149
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 60/127,032
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 1489
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 US-10-266-041-9

Query Match 93.9%; Score 1228; DB 15; Length 1489;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

1 ATGAAAGCATCTTAATCCATTTTATCTCTCTGATCCGTTAACCCCGCAATCTGCA 60
 182 ATGAAAGCATCTTAATCCATTTTATCTCTCTGATCCGTTAACCCCGCAATCTGCA 241
 61 TTGCTCAGAGTAGCCCGAGCTGAAAGTGTGTGATTTGTCACTGCTCATGTGT 120
 242 TTGCTCAGAGTAGCCCGAGCTGAAAGTGTGTGATTTGTCACTGCTCATGTGT 301
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 302 GTGCTGCTCCAAACCAAGGCCAAGCACTGATGAGATGTCACCCCAAGAGATGCCA 361
 181 ACTGCGCGGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTGCTATCTC 240
 362 ACTGCGCGGTAAATGAGTGAAGCTGACACCGCGCGTGTGAGTAACTGCTATCTC 421
 241 GGAATTAATCTGAGCTCAGCTGTGTGAGCCGACGATTTGCTCTAAATGTGTGCTCC 300

Db 422 GGAATTACCAAGCCGCTGCTGCGCCGAGGATTCGTGCGAAGAAAAGCGTCGCCG 481
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 Db 482 CAGCTGGTCAAGTCCGCGATTTATGCTGATGTCAGAGCGTACCCGTAACAGAGCGAA 541
 QY 361 GCCTTGGCCCGCGCGGCTGCGACCCGACTGTCGATTAACCGTAACACCGAGAGATAG 420
 Db 542 GCCTTGGCCCGCGCGGCTGCGACCCGACTGTCGATTAACCGTAACACCGAGAGATAG 601
 QY 421 TCCAGTCCCGATCCGTTATTTATCTCTAATAAACTGCGCTTTCGCAATGATAACGCG 480
 Db 602 TCCAGTCCCGATCCGTTATTTATCTCTAATAAACTGCGCTTTCGCAATGATAACGCG 661
 QY 481 AACGTGACTGACGGATTCCTCGAAGAGGCGAGAGGTCATTCGTGACTTAACCGGCGAT 540
 Db 662 AACGTGACTGACGGATTCCTCGAAGAGGCGAGAGGTCATTCGTGACTTAACCGGCGAT 721
 QY 541 TATCAAAAGCGGCTTTCGCGAATGGAACGAGTGTCTAATTTCCGCAATCAAACTTGTGC 600
 Db 722 CGGCAAAAGCGGCTTTCGCGAATGGAACGAGTGTCTAATTTCCGCAATCAAACTTGTGC 781
 QY 601 CTTAACCTGTAAGAAACAGAGAAAGCTGTTCAATTAACGAGGATTAACCATCGGAATC 660
 Db 782 CTTAACCTGTAAGAAACAGAGAAAGCTGTTCAATTAACGAGGATTAACCATCGGAATC 841
 QY 661 AAGGTGACGCGCGACTGTGTCTCATTAACGCGGTGCGTAAGCTCGCATCAATCTGACG 720
 Db 842 AAGGTGACGCGCGACTGTGTCTCATTAACGCGGTGCGTAAGCTCGCATCAATCTGACG 901
 QY 721 GAGATATTTCTCTGCAACAAAGCAAGGGAATGCCGAGCCGCGGTGGGAAAGATCAAC 780
 Db 902 GAAATATTTCTCTGCAACAAAGCAAGGGAATGCCGAGCCGCGGTGGGAAAGATCAAC 961
 QY 781 GATTCAACCAAGTGAACACCTTGTGTAAGTTGCAATTAACGCGCAATTTGATTCTCAAA 840
 Db 962 GATTCAACCAAGTGAACACCTTGTGTAAGTTGCAATTAACGCGCAATTTGATTCTCAAA 1021
 QY 841 CGCAGCGCAAGTGTCCCGCAGCCGCGCACCCCGCTATTATTAAGTTGATCAACAGCG 900
 Db 1022 CGCAGCGCAAGTGTCCCGCAGCCGCGCACCCCGCTATTATTAAGTTGATCAACAGCG 1081
 QY 901 TTGACGCGCCCATCAACCGCAAAAGCGGTATGCTGATTAACCACTTCAGTCTG 960
 Db 1082 TTGACGCGCCCATCAACCGCAAAAGCGGTATGCTGATTAACCACTTCAGTCTG 1141
 QY 961 TTTATCGCGGACACGATTAATCTGCAAACTCTGCGCGCGCACTGAGACTCACTG 1020
 Db 1142 TTTATCGCGGACACGATTAATCTGCAAACTCTGCGCGCGCACTGAGACTCACTG 1201
 QY 1021 AGCTTCCCGCTCAACCGGATTAACGCGCGCAAGTGTGTAACGTTGTTGAACGCTG 1080
 Db 1202 AGCTTCCCGCTCAACCGGATTAACGCGCGCAAGTGTGTAACGTTGTTGAACGCTG 1261
 QY 1081 CGTCCGCTAAGGATTAACGCGGATTAACGAGTTTCAGTGTCTGCTTCAGACTTTAAG 1140
 Db 1262 CGTCCGCTAAGGATTAACGCGGATTAACGAGTTTCAGTGTCTGCTTCAGACTTTAAG 1321
 QY 1141 CAGATGCGGTATTAACGCGGCTGCTCATTTAATAGCCGCCCGGAGAGATTAAGTACC 1200
 Db 1322 CAGATGCGGTATTAACGCGGCTGCTCATTTAATAGCCGCCCGGAGAGATTAAGTACC 1381
 QY 1201 CTGGCAGGATGTAAGAGGAAATGCGAGGCGCATGTTCTGTTGGCAGGTTTACGCA 1260
 Db 1382 CTGGCAGGATGTAAGAGGAAATGCGAGGCGCATGTTCTGTTGGCAGGTTTACGCA 1441
 QY 1261 ATCGTGAATGAAGCAAGCATACCGCGCTGCACTTTGAAT 1300
 Db 1442 ATCGTGAATGAAGCAAGCATACCGCGCTGCACTTTGAAT 1481

RESULT 13
 US-10-284-962-1

; Sequence 1, Application US/10284962
 ; Publication No. US20030206913A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weibel, Douglas M.
 ; APPLICANT: Orr, Donald E.
 ; APPLICANT: Ruch, Frank E.
 ; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
 ; FILE REFERENCE: 834460-71725
 ; CURRENT APPLICATION NUMBER: US/10/284,962
 ; PRIOR FILING DATE: 2002-10-31
 ; PRIOR FILING DATE: 2001-10-31
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO. 1
 ; LENGTH: 1489
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: (1)..(22)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: (1468)..(1489)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (16)..(108)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (182)..(1480)
 ; OTHER INFORMATION:
 ; US-10-284-962-1
 Query Match 93.9%; Score 1228; DB 16; Length 1489;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 ATGAAGCATCTTAATCCCATTTTATCTCTTCGATTCCTGTTAACCCCGCAATCTGCA 60
 Db 182 ATGAAGCATCTTAATCCCATTTTATCTCTTCGATTCCTGTTAACCCCGCAATCTGCA 241
 QY 61 TTGGCTCAAGTGAAGCGGAGCTGAAGTGAAGTGTGATGATGTCATGAT 120
 Db 242 TTGGCTCAAGTGAAGCGGAGCTGAAGTGAAGTGTGATGATGTCATGAT 301
 QY 121 GTGCGTCTCCAAACCAAGGCCAGCACTGATGCAAGATGTCAACCCAGAGCATGGCA 180
 Db 302 GTGCGTCTCCAAACCAAGGCCAGCACTGATGCAAGATGTCAACCCAGAGCATGGCA 361
 QY 302 GTGCGTCTCCAAACCAAGGCCAGCACTGATGCAAGATGTCAACCCAGAGCATGGCA 361
 Db 181 ACCTGCGCGTAAATCTGGGTGAGTGAACGCGCGGTGAGCTAATCGCTATCTC 240
 QY 241 ACCTGCGCGTAAATCTGGGTGAGTGAACGCGCGGTGAGCTAATCGCTATCTC 300
 Db 362 ACCTGCGCGTAAATCTGGGTGAGTGAACGCGCGGTGAGCTAATCGCTATCTC 421
 QY 422 GGAATTACCAAGCGCAGCGTCTGCTGAGCGGATTCGCTAATGTCGTCGCG 481
 Db 482 GGAATTACCAAGCGCAGCGTCTGCTGAGCGGATTCGCTAATGTCGTCGCG 481
 QY 301 CAGTCTGTCAGGTCCGCAATTAATGCTGATGTCAGAGCGTAAACCGGTAACAGCGAA 360
 Db 482 CAGTCTGTCAGGTCCGCAATTAATGCTGATGTCAGAGCGTAAACCGGTAACAGCGAA 541
 QY 361 GCCTTGGCCCGCGGCTGCGACCTGACTGTGCAATTAACCGTAAATCCAGGAGATAG 420
 Db 542 GCCTTGGCCCGCGGCTGCGACCTGACTGTGCAATTAACCGTAAATCCAGGAGATAG 601
 QY 421 TCCAGTCCCGATCCGTTATTTATCTCTAATAAACTGCGCTTTCGCAATGATAACGCG 480
 Db 602 TCCAGTCCCGATCCGTTATTTATCTCTAATAAACTGCGCTTTCGCAATGATAACGCG 661
 QY 481 AACGTGACTGACGGATTCCTCGAAGAGGCGAGAGGTCATTCGTGACTTAACCGGCGAT 540

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Db 662 AACGTGACGCGATCTGACGAGGAGGAGGATGCTGATCTTACCGGGCAT 721
Qy 541 TATCAAAACGCGGTTTCGGAACGGAACGAGGCTTAAATTTCCGCAATCAACTTGTGC 600
Db 722 CGGCAACGCGGTTTCGGAACGGAACGAGGCTTAAATTTCCGCAATCAACTTGTGC 781
Qy 601 CTTAAACGTGAGAAACAGGAAAGCTGTTCAATTAACGAGGCAATTAACGAGAACTC 660
Db 782 CTTAAACGTGAGAAACAGGAAAGCTGTTCAATTAACGAGGCAATTAACGAGAACTC 841
Qy 661 AAGGTGACGCGGATGCTGCTCATTTAACCGGTGCGGTAACCTCGCATCACTGACG 720
Db 842 AAGGTGACGCGGATGCTGCTCATTTAACCGGTGCGGTAACCTCGCATCACTGACG 901
Qy 721 GAGATATTTCTCTGCAACAGGCAAGGAAATGCGGAGCGGAGGAGGAGATCAC 780
Db 902 GAAATATTTCTCTGCAACAGGCAAGGAAATGCGGAGCGGAGGAGGAGATCAC 961
Qy 781 GATTCAACACGATGGAACACCTGCTAGTTGCAATACGCGCAATTTGATTGCTACAA 840
Db 962 GATTCAACACGATGGAACACCTGCTAGTTGCAATACGCGCAATTTGATTGCTACAA 1021
Qy 841 CGACGCGGAGGTTGCGCGGACGCGGCGCACCCCGTTATTAGATTGATCAGACGCG 900
Db 1022 CGACGCGGAGGTTGCGCGGACGCGGCGCACCCCGTTATTAGATTGATCAGACGCG 1081
Qy 901 TTGAGCGCGGATCCGACCGGCAAAACAGGCGATAGTGATGATTAACCACTTCAGTGTG 960
Db 1082 TTGAGCGCGGATCCGACCGGCAAAACAGGCGATAGTGATGATTAACCACTTCAGTGTG 1141
Qy 961 TTATATCGCGGACGATATCTATCTGCAATCTCGCGGCGCATGAGACTCACTG 1020
Db 1142 TTATATCGCGGACGATATCTATCTGCAATCTCGCGGCGCATGAGACTCACTG 1201
Qy 1021 ACGCTTCCCGGTCACCGGATTAACCGCGGCGCATGAGACTGATGATTTGAACGCTG 1080
Db 1202 ACGCTTCCCGGTCACCGGATTAACCGCGGCGCATGAGACTGATGATTTGAACGCTG 1261
Qy 1081 CGTCGCGGATGAGGATTAACGCGGCGCATGAGACTGATGATTTGAACGCTG 1140
Db 1262 CGTCGCGGATGAGGATTAACGCGGCGCATGAGACTGATGATTTGAACGCTG 1321
Qy 1141 CAGATGCGGATTAACGCGGCGCATGATTAACGCGGCGCATGAGACTGATGATTTGAACGCTG 1200
Db 1322 CAGATGCGGATTAACGCGGCGCATGATTAACGCGGCGCATGAGACTGATGATTTGAACGCTG 1381
Qy 1201 CTGGGAGATGAGGAGGAAATGCGGAGGCGATGATGATTTGAACGCTG 1260
Db 1382 CTGGGAGATGAGGAGGAAATGCGGAGGCGATGATGATTTGAACGCTG 1441
Qy 1261 ATCGTGAATGAAGCAGCATACCGGCGTGCAGTTGAGAT 1300
Db 1442 ATCGTGAATGAAGCAGCATACCGGCGTGCAGTTGAGAT 1481

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; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (188) ..(1483)
; OTHER INFORMATION:
US-10-284-962-4

Query Match 93.5%; Score 1222.4; DB 16; Length 1486;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1250; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 ATGAAGCATCTATATCCATTTTATCTCTGATATCCGTTAACCAGCATCTGCA 60
Db 188 ATGAAGCATCTATATCCATTTTATCTCTGATATCCGTTAACCAGCATCTGCA 247
Qy 61 TTGCTCAGAGTGAAGCGGAGCTGAAGTGAAGTGTGATTTGATGCTCATGCT 120
Db 248 TTGCTCAGAGTGAAGCGGAGCTGAAGTGAAGTGTGATTTGATGCTCATGCT 307
Qy 121 GTGCGTCTCCAAACGAGGCGCAACGCACTGATGAGGATGTCACCCAGAGCATGGCA 180
Db 308 GTGCGTCTCCAAACGAGGCGCAACGCACTGATGAGGATGTCACCCAGAGCATGGCA 367
Qy 181 ACCTGCGCGGTAACCTGAGTGAAGCTGACACCGCGGATGATGAGCTAATGCTATCTC 240
Db 368 ACCTGCGCGGTAACCTGAGTGAAGCTGACACCGCGGATGATGAGCTAATGCTATCTC 427
Qy 241 GGCATTTATCGAGGTGAGGCTCTGATGAGGCGGATGCTGCTAATGAGGCTGCGCG 300
Db 428 GGCATTTATCGAGGTGAGGCTCTGATGAGGCGGATGCTGCTAATGAGGCTGCGCG 487
Qy 301 CAGCTGTGATGAGTCCGATTTATGCTGATGTCAGAGCGTACCCGTAAACAGGCGAA 360
Db 488 CAGCTGTGATGAGTCCGATTTATGCTGATGTCAGAGCGTACCCGTAAACAGGCGAA 547
Qy 361 GCTTGTGCGCGCGGCTGCGACTGATGTCATACCTGATACCTGATACCTGATAC 420
Db 548 GCTTGTGCGCGCGGCTGCGACTGATGTCATACCTGATACCTGATACCTGATAC 607
Qy 421 TCCAGTCCCGATCGTATTTTAACTCTTAAACAGGCGGCTTGGCAATCTGATTAACGCG 480
Db 608 TCCAGTCCCGATCGTATTTTAACTCTTAAACAGGCGGCTTGGCAATCTGATTAACGCG 667
Qy 481 AACGTGATGACGCGATCTCTGAGAGGCGAGAGGCTCAATTGCTGATCTTAACCGGCAAT 540
Db 668 AACGTGATGACGCGATCTCTGAGAGGCGAGAGGCTCAATTGCTGATCTTAACCGGCAAT 727
Qy 541 TATCAAAACGCGGTTTCGGAACGGAACGAGGCTTAAATTTCCGCAATCAACTTGTGC 600
Db 728 CGGCAACGCGGTTTCGGAACGGAACGAGGCTTAAATTTCCGCAATCAACTTGTGC 787
Qy 601 CTTAAACGTGAGAAACAGGAAAGCTGTTCAATTAACGAGGCAATTAACGAGAACTC 660
Db 788 CTTAAACGTGAGAAACAGGAAAGCTGTTCAATTAACGAGGCAATTAACGAGAACTC 847
Qy 661 AAGGTGACGCGGATGCTGCTCATTTAACCGGTGCGGTAACCTCGCATCACTGACG 720
Db 848 AAGGTGACGCGGATGCTGCTCATTTAACCGGTGCGGTAACCTCGCATCACTGACG 907
Qy 721 GAGATATTTCTCTGCAACAGGCAAGGAAATGCGGAGCGGAGGAGGAGATCAC 780
Db 908 GAAATATTTCTCTGCAACAGGCAAGGAAATGCGGAGCGGAGGAGGAGATCAC 967
Qy 781 GATTCAACACGATGGAACACCTGCTAGTTGCAATTAACGCGCAATTTGATTGCTACAA 840
Db 968 GATTCAACACGATGGAACACCTGCTAGTTGCAATTAACGCGCAATTTGATTGCTACAA 1027
Qy 841 CGACGCGGAGGTTGCGCGGACGCGGCGCACCCCGTTATTAGATTGATCAAGACGCG 900
Db 1028 CGACGCGGAGGTTGCGCGGACGCGGCGCACCCCGTTATTAGATTGATCAAGACGCG 1087

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RESULT 14
US-10-284-962-4
; Sequence 4, Application US/10284962
; Publication No. US20030206913A1
; GENERAL INFORMATION:
; APPLICANT: Weibel, Douglas M.
; APPLICANT: Orr, Donald E.
; APPLICANT: Ruch, Frank E.
; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
; FILE REFERENCE: 834460-71/25
; CURRENT APPLICATION NUMBER: US/10/284,962
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/335,303
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4

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QY 901 TTGAGCCCATTCACCGCAAAAACAGCGTATGATGTGACATTACCACTTCACTGCTG 960
 Db 1088 TTGAGCCCATTCACCGCAAAAACAGCGTATGATGTGACATTACCACTTCACTGCTG 1147
 QY 961 TTTATGCGCGGACGACGATCTAATCTGCGCAAACTCGCGCGGACGACGACGCTCACTG 1020
 Db 1148 TTTATGCGCGGACGACGATCTAATCTGCGCAAACTCGCGCGGACGACGACGCTCACTG 1207
 QY 1021 ACCGTCCTCCGCTACGCGGATTAACAGCGCGGACGAGTGAATCTGTTTGAACGCTG 1080
 Db 1208 ACCGTCCTCCGCTACGCGGATTAACAGCGCGGACGAGTGAATCTGTTTGAACGCTG 1267
 QY 1081 CGTGGCTTAAGCGATTAACAGCGGATTAACAGCGGCTGCTGCTGCTGCTGCTGCTG 1140
 Db 1268 CGTGGCTTAAGCGATTAACAGCGGATTAACAGCGGCTGCTGCTGCTGCTGCTGCTG 1327
 QY 1141 CAGATGCGTGAATAAAGCGCGCTGCTCATTAATACGCGCGCGGAGAGTGAATCTGACC 1200
 Db 1328 CAGATGCGTGAATAAAGCGCGCTGCTCATTAATACGCGCGCGGAGAGTGAATCTGACC 1387
 QY 1201 CTGGCAGATGTGAAGACCGCAATCCGCAAGGCACTGTTCTGTTGCGAGGTTTAAAGCA 1260
 Db 1388 CTGGCAGATGTGAAGACCGCAATCCGCAAGGCACTGTTCTGTTGCGAGGTTTAAAGCA 1447
 QY 1261 ATCGTGAATGAAGACGATACCGGCGTGCAGTTTG 1296
 Db 1448 ATCGTGAATGAAGACGATACCGGCGTGCAGTTTG 1483

RESULT 15

US-10-334-672-4
 ; Sequence 4, Application US/10334672
 ; Publication No. US20030157646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larnahan, Mike
 ; APPLICANT: Koepf, Edward
 ; APPLICANT: Kretz, Keith
 ; TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phylase For Animal Feed
 ; FILE REFERENCE: SYNG-P01-001
 ; CURRENT APPLICATION NUMBER: US/10/334,672
 ; PRIOR FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: 60/344,523
 ; PRIOR FILING DATE: 2001-12-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 1281
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. US20030157646A19X gene
 US-10-334-672-4

Query Match 52.9%; Score 691.4; DB 15; Length 1281;
 Best Local Similarity 72.4%; Pred. No. 8,1e-233;
 Matches 896; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

QY 64 GCTCAAGTGAAGCGGAGCTGAAGCTGGAAGTGTGGTATGTCAGTCTGATGCTG 123
 Db 28 GCTCAATCTGAACCAAGATTGAAGTGTGAATCTGTTCATTTGCTCAAGCAAGGTT 87
 QY 124 CGTGCTCAACCAAGGCGCAAGCTGATGCAAGATGTCACCCAGACGATGCGCAAC 183
 Db 88 AGAGTCCAACTAAGGCTACTCAAGTATGCAAGATGTTACTCAAGATGCTGCGCTAAC 147
 QY 184 TGGCGGTGAAGAACTGGGTGAGCTGACACCGCGCGGTGTGAGCTTAATGCTTACTGGA 243
 Db 148 TGGCGGTGAAGTGGGTGAATGATCTCCAAAGAGTGTGAATGATGCTTACTTGGGT 207
 QY 244 CATTAAGTGAAGCTGCTGATGAGCGGACGATTTGCTTAATATGCTGCGCGGAG 303
 Db 208 CATTAAGTGAAGAAAGTGTGCTGATGCTTGTTCCTCAAGTGTGCTGCTCAAA 267

QY 304 TCTGCTCAGTGGCGGATTAATGCTGATGTGACAGAGGATCCGTAATAACAGCGGAAGCC 363
 Db 268 TCTGCTCAGTGGCGGATTAATGCTGATGTGATGATGATGATGATGATGATGATGATGATG 327
 QY 364 TTTGCGCGCGGCGTGGCACTGATGCTGATTAACCGTATACCCAGGAGATACGCTCC 423
 Db 328 TTTGCGCGCGGTTTGCGCGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 387
 QY 424 AGTCCGATTCGCTTAATTAATCTGTAATAAATCGCGCTTGGCCACTGATTAAGCCGAC 483
 Db 388 TCTCCAGATTCATGCTTAATTAATGATTAAGATGATGATGATGATGATGATGATGATGATG 447
 QY 484 GTGATGACGCGGATCTGAGAGGCGAGAGGATCAATGCTGATTAACCGGCAATTAAT 543
 Db 448 GTTACTGATGCTGATTTGGAAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 507
 QY 544 CAACGCGGCTTTCGGAATGGAACGAGTGTCTTAATTTTCCGCAATCAACTTGTGCTT 603
 Db 508 CAACGCGCTTCAAGAAATGGAAGAGTGTGAACTTCCCAATCAATCACTTGTGCTT 567
 QY 604 AAACGTGAAGAAACAGAGAGAAAGCTGCTTAATTAACGAGGATTAACATCGGAATCAAG 663
 Db 568 AAAGAGAGAGAGAGAGAGAGATCTTGTCTGATGATGATGATGATGATGATGATGATGATGATG 627
 QY 664 GTGAGCGCGGATGCTGCTCATTAACCGGTGCGGTAAAGCTTCGATCAATGCTGACGAG 723
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 QY 724 ATATTTCTCTGCAACAGACAGAGGATGCGGAGCGCGGCGGAGAGATCAACGAT 783
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 Db 748 TCTCAACATGGAACACCTGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807
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 Db 808 ACTCCAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 867
 QY 904 AGCGGAGATGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 963
 Db 868 ACTCCAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 927
 QY 964 ATGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 1023
 Db 928 ATGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 987
 QY 1024 CTTCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 1083
 Db 988 TTGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 1047
 QY 1084 CGGCTAAGCGATTAACAGCGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1143
 Db 1108 ATGAGAGCAAGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1167
 QY 1204 GAGAGATGGAAGAGCAAGATGCGAGGCGATGTTGTTGCGAGGTTTAAAGCAATTC 1263
 Db 1168 GCTGTTGTTGAAGAAAGAGCTCAAGTATGTTTCTTGGCTGAGTTTCACTCAATTC 1227
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 Db 1228 GTGAAGAGCAAGATTAACCGGCGGAGCTTGAAT 1264

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 21:37:37 ; Search time 104.347 Seconds
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Title: US-09-866-379D-9

Perfect score: 1308

Sequence: 1 atgaagcgcactcaatcc.....gcagttcgagatcactca 1308

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1265	96.7	1323	3	US-09-318-528-1
3	1265	96.7	1323	3	US-09-291-931-1
4	1228	93.9	1489	4	US-09-540-149A-9
5	1153	88.1	1272	2	US-08-910-798-1
6	66.2	5.1	1266	4	US-09-489-039A-341
7	39.8	3.0	505	4	US-09-621-976-15639
8	36.6	2.8	2868	4	US-09-710-794-4
9	34.4	2.6	4403765	3	US-09-103-840A-2
10	34.4	2.6	4411529	3	US-09-103-840A-1
11	34.2	2.6	4403765	3	US-09-103-840A-2
12	34.2	2.6	4411529	3	US-09-103-840A-1
13	34	2.6	998	2	US-07-885-089B-5
14	33.8	2.6	399	4	US-09-621-976-8976
15	33	2.5	2511	2	US-08-680-326-116
16	33	2.5	35100	2	US-08-770-379-17
17	33	2.5	35100	3	US-08-757-668A-17
18	33	2.5	35100	4	US-09-230-371A-17
19	32.6	2.5	3147	1	US-08-441-430-3
20	32.6	2.5	4485	4	US-09-023-655-1286
21	32.6	2.5	4488	1	US-08-441-430-1
22	32.2	2.5	2430	4	US-09-489-039A-1732
23	32.2	2.5	3076	4	US-09-710-794-1
24	32	2.4	1533	4	US-09-489-039A-607
25	31.8	2.4	474	4	US-09-621-976-18033
26	31.8	2.4	480	4	US-09-252-991A-15917
27	31.8	2.4	762	4	US-09-252-991A-15888

C 28	31.8	2.4	885	4	US-09-252-991A-15774	Sequence 15774, A
C 29	31.8	2.4	1068	4	US-09-252-991A-15804	Sequence 15804, A
C 30	31.6	2.4	505	4	US-09-621-976-15639	Sequence 15639, A
C 31	31.2	2.4	825	4	US-09-489-039A-172	Sequence 172, App
C 32	31.2	2.4	1034	4	US-09-072-596-312	Sequence 312, App
C 33	31.2	2.4	1034	4	US-09-072-596-317	Sequence 317, App
C 34	31	2.4	498	4	US-09-252-991A-7289	Sequence 7289, Ap
C 35	31	2.4	966	4	US-09-252-991A-7468	Sequence 7468, Ap
C 36	31	2.4	1329	4	US-09-489-039A-3268	Sequence 3268, Ap
C 37	31	2.4	1563	4	US-09-252-991A-7226	Sequence 7226, Ap
C 38	31	2.4	1734	4	US-08-857-636-58	Sequence 58, App1
C 39	31	2.4	3753	5	PCT-US95-02251-2	Sequence 2, App1
C 40	31	2.4	3759	3	US-08-479-722B-3	Sequence 3, App1
C 41	31	2.4	4314	1	US-08-199-780-2	Sequence 2, App1
C 42	31	2.4	4314	2	US-08-316-780-2	Sequence 2, App1
C 43	30.8	2.4	1491	4	US-09-540-236-920	Sequence 920, App
C 44	30.8	2.4	94750	4	US-09-596-002-38	Sequence 38, App1
C 45	30.6	2.3	1086	4	US-09-489-039A-3528	Sequence 3528, Ap

ALIGNMENTS

RESULT 1
US-09-259-214-1
Sequence 1, Application US/09259214A
Patent No. 6110719
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVER1370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or G
US-09-259-214-1

Query Match 96.7%; Score 1265; DB 3; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	1	ATGAAGCAGTCTTAATCCATTTTATCTCTGATTCGGTTAACCCGCAATTCGA	60
DB	1	ATGAAGCAGTCTTAATCCATTTTATCTCTGATTCGGTTAACCCGCAATTCGA	60
QY	61	TTGCTCAGAGTGAAGCCGAGTGAAGCTGGAAGAGTGTGATTTCTGCTCATGGT	120
DB	61	TTGCTCAGAGTGAAGCCGAGTGAAGCTGGAAGAGTGTGATTTCTGCTCATGGT	120
QY	121	GTGGGTGCTCAACAGGCGACGCAACTGATGACAGATGTACACCCGACGATGCGCA	180
DB	121	GTGGGTGCTCAACAGGCGACGCAACTGATGACAGATGTACACCCGACGATGCGCA	180
QY	181	ACCTGGCGGTAAACTGTGAGTGAACCGCGGCTGTGAGCTAATCGCTATCTTC	240
DB	181	ACCTGGCGGTAAACTGTGAGTGAACCGCGGCTGTGAGCTAATCGCTATCTTC	240
QY	241	GGAATTACGAGGTGAGGCTGAGGCTGAGGCGAGATGCTGCTTAATGTGGCTGCCG	300
DB	241	GGAATTACGAGGTGAGGCTGAGGCTGAGGCGAGATGCTGCTTAATGTGGCTGCCG	300

301 CAGCTGTGAGGTCGCGATTTATTTGATGTGAGAGGAGTACCCGGTAAACAGAGCGAA 360
301 CAGCTGTGAGGTCGCGATTTATTTGATGTGAGAGGAGTACCCGGTAAACAGAGCGAA 360
361 GCCTTCGCGCGCGGCTGAGCACTGACTGTGCAATTAACGTAATACCAAGAGATAGC 420
361 GCCTTCGCGCGCGGCTGAGCACTGACTGTGCAATTAACGTAATACCAAGAGATAGC 420
421 TCCAGTCCGATTCGGTATTTATTTATCTCTTAATACTGGCGCTTGGCCCACTGGATTAACG 480
421 TCCAGTCCGATTCGGTATTTATTTATCTCTTAATACTGGCGCTTGGCCCACTGGATTAACG 480
481 AACGTGACTGACGCGATCTCTGAGAGAGGAGGAGGAGTCAATTGCTGACTTTACCGGCGAT 540
481 AACGTGACTGACGCGATCTCTGAGAGAGGAGGAGGAGTCAATTGCTGACTTTACCGGCGAT 540
541 TATTAACAGCGGCTTTCGCGAACTGGAACGGGCTTAAATTTTCGCGATCAAACTTGTGC 600
541 TATTAACAGCGGCTTTCGCGAACTGGAACGGGCTTAAATTTTCGCGATCAAACTTGTGC 600
601 CTTAAACGTGAGAAACAGAGCAAGAGTGTTCATTAAAGCAAGGATTAACCATTCGAACTC 660
601 CTTAAACGTGAGAAACAGAGCAAGAGTGTTCATTAAAGCAAGGATTAACCATTCGAACTC 660
661 AAGGTGAGCGCGGCTGTGTCTCAATTAACGGGTGCGGTAAAGCTTCGATCAATGCTGAGC 720
661 AAGGTGAGCGCGGCTGTGTCTCAATTAACGGGTGCGGTAAAGCTTCGATCAATGCTGAGC 720
721 GAGATATTTCTCTCGCAACAAAGCAAGGAGTACCGGAGCGGGGTGGGAGGATCAAC 780
721 GAGATATTTCTCTCGCAACAAAGCAAGGAGTACCGGAGCGGGGTGGGAGGATCAAC 780
781 GATTCAACCAAGTGAACACCTTCTTAAGTTGCAATTAACGGGCAATTTGATTTGCTACAA 840
781 GATTCAACCAAGTGAACACCTTCTTAAGTTGCAATTAACGGGCAATTTGATTTGCTACAA 840
841 CGCAGCGCAGAGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
841 CGCAGCGCAGAGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
901 TTGAAGCGCCCATTCACCGCAAAACAGGCGGTATGTGATTAACCACTTCAGTGTCTG 960
901 TTGAAGCGCCCATTCACCGCAAAACAGGCGGTATGTGATTAACCACTTCAGTGTCTG 960
961 TTATATGCGCGGAGCAAGTAACTTAATCTGCAAAATCTGCGCGGCGGCACTGAGCTCAATG 1020
961 TTATATGCGCGGAGCAAGTAACTTAATCTGCAAAATCTGCGCGGCGGCACTGAGCTCAATG 1020
1021 ACGCTTCGCGGCTGACGCGGATTAACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
1021 ACGCTTCGCGGCTGACGCGGATTAACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
1081 ACGCTTCGCGGCTGACGCGGATTAACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
1081 ACGCTTCGCGGCTGACGCGGATTAACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
1141 CAGATGCGGTGATTAACGCGCGGCTGTCAATTAATAGCGCGCGCGGAGGAGTAACTGACC 1200
1141 CAGATGCGGTGATTAACGCGCGGCTGTCAATTAATAGCGCGCGCGGAGGAGTAACTGACC 1200
1201 CTGCGCAGATGTGAAGAGCAAAATGCGAGGCGCATGTGTTGCGGAGGTTTAACTGCAA 1260
1201 CTGCGCAGATGTGAAGAGCAAAATGCGAGGCGCATGTGTTGCGGAGGTTTAACTGCAA 1260
1261 ATCGTGAATGAAGCAAGCATACCGGCGGTGCAATTGAGATCTCATC 1306
1261 ATCGTGAATGAAGCAAGCATACCGGCGGTGCAATTGAGATCTCATC 1306

GENERAL INFORMATION:
APPLICANT: Kreiz, Keith
TITLE OF INVENTION: NOVEL PHRASE
FILE REFERENCE: 09/010/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
SOFTWARE: FastSeq for Windows Version 4.0
SEO ID NO. 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or G
US-09-318-528-1

Query Match 96.7%; Score 1265; DB 3; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

1 ATGAAGAGGATCTTATCCATTTTATCTTCTGATTCGGTAAACCGGCAATTCGCA 60
1 ATGAAGAGGATCTTATCCATTTTATCTTCTGATTCGGTAAACCGGCAATTCGCA 60
61 TTGCTCAGAGTGAACCGGAGTGAAGTGAAGTGTGATTCAGTTCATGAT 120
61 TTGCTCAGAGTGAACCGGAGTGAAGTGAAGTGTGATTCAGTTCATGAT 120
121 GTGCTGTCTCCACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
121 GTGCTGTCTCCACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
181 ACCCTGCGGCTTAACTGAGTGAAGTGAAGTGAAGTGTGATTCAGTTCATGAT 240
181 ACCCTGCGGCTTAACTGAGTGAAGTGAAGTGAAGTGTGATTCAGTTCATGAT 240
241 GGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
241 GGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
301 CAGTCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360
301 CAGTCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360
361 GCCTTCGCGCGCGGCTGAGCACTGACTGTGCAATTAACGTAATACCAAGAGATAGC 420
361 GCCTTCGCGCGCGGCTGAGCACTGACTGTGCAATTAACGTAATACCAAGAGATAGC 420
421 TCCAGTCCGATTCGGTATTTATTTATCTCTTAATACTGGCGCTTGGCCCACTGGATTAACG 480
421 TCCAGTCCGATTCGGTATTTATTTATCTCTTAATACTGGCGCTTGGCCCACTGGATTAACG 480
481 AACGTGACTGACGCGATCTCTGAGAGAGGAGGAGGAGTCAATTGCTGACTTTACCGGCGAT 540
481 AACGTGACTGACGCGATCTCTGAGAGAGGAGGAGGAGTCAATTGCTGACTTTACCGGCGAT 540
541 TATTAACAGCGGCTTTCGCGAACTGGAACGGGCTTAAATTTTCGCGATCAAACTTGTGC 600
541 TATTAACAGCGGCTTTCGCGAACTGGAACGGGCTTAAATTTTCGCGATCAAACTTGTGC 600
601 CTTAAACGTGAGAAACAGAGCAAGAGTGTTCATTAAAGCAAGGATTAACCATTCGAACTC 660
601 CTTAAACGTGAGAAACAGAGCAAGAGTGTTCATTAAAGCAAGGATTAACCATTCGAACTC 660

Qy	66	AAGGAGAGGCGCGCATGTGTCTCATTTAACCGGTGGGTAACCTCGCATCAATGCTGACG	720
Dp	661	AAGGAGAGGCGCGCATGTCTCATTTAACCGGTGGGTAACCTCGCATCAATGCTGACG	720
Qy	721	GAGATTTTCTCTCTGCAACAGCAACAGGAATGCCCGAGCCGGGTGGGAAAGATCAC	780
Dp	721	GAGATTTTCTCTCTGCAACAGCAACAGGAATGCCCGAGCCGGGTGGGAAAGATCAC	780
Qy	781	GATTCAACACAGTGGNAACATTCTGTAAGTTGGCTAAACGGCAATTTGATTGGCTACAA	840
Dp	781	GATTCAACACAGTGGNAACATTCTGTAAGTTGGCTAAACGGCAATTTTATTGGCTACAA	840
Qy	841	CGACGCGCAGAGTTGCCCCGACGCGCGCACCCCGTTATTAGATTGATCAAGACAGCG	900
Dp	841	CGACGCGCAGAGTTGCCCCGACGCGCGCACCCCGTTATTGATTTGATTCATGGCAGCG	900
Qy	901	TTGACGCCCATTCACACCGCAAAAAGGCGATGGGTGTGACATTAAACCACTTCAGTGTG	960
Dp	901	TTGACGCCCATTCACACCGCAAAAAGGCGATGGGTGTGACATTAAACCACTTCAGTGTG	960
Qy	961	TTTATGCGCGGACACAGATCTAATCTGCGAAATCTCGCGCGGCACTGAGACTCAATGG	1020
Dp	961	TTTATTTCCGACACAGATCTAATCTGCGAAATCTCGCGCGGCACTGAGACTCAATGG	1020
Qy	1021	ACGCTTCCCGGTCAACGCGGATPACACGCGCGCAGGTGTGAATCTGGTGTGAACGCTGG	1080
Dp	1021	ACGCTTCCCGGTCAACGCGGATPACACGCGCGCAGGTGTGAATCTGGTGTGAACGCTGG	1080
Qy	1081	CGTCCGCTAAGCGATPACAGCAGATGAGTTCAGTTCGCGGTCTTCAGACTTTACAG	1140
Dp	1081	CGTCCGCTAAGCGATPACAGCAGATGAGTTCAGTTCGCGGTCTTCAGACTTTACAG	1140
Qy	1141	CAGATGCGTGAATPAAAACGCCGCTGTCTATTAAATACGCCCGCGGAGAGGTGAACCTAAC	1200
Dp	1141	CAGATGCGTGAATPAAAACGCCGCTGTCTATTAAATACGCCCGCGGAGAGGTGAACCTAAC	1200
Qy	1201	CTGGCAGAGATGTGANAAGCGAAATGCGCAGGCGCATGTTCGTTGGCAGGTTTACGCAA	1260
Dp	1201	CTGGCAGAGATGTGANAAGCGAAATGCGCAGGCGCATGTTCGTTGGCAGGTTTACGCAA	1260
Qy	1261	ATGCTGAATGAACACAGCATACCGCGGTGCAATTTGAAATCTCAATC	1306
Dp	1261	ATGCTGAATGAACACAGCATACCGCGGTGCAATTTGAAATCTCAATC	1306

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RESULT 3
US-09-291-931-1
Sequence 1, Application US/09291931A
Patent No. 6190697
GENERAL INFORMATION:
APPLICANT: Kretz, Neilh
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/028003
CURRENT APPLICATION NUMBER: US/09/291,931-1
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (1320)
NAME/KEY: misc feature
LOCATION: (1) _ (1323)
OTHER INFORMATION: n = A,T,C or G
US-09-291-931-1

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Query Match	Similarity	96.7%	Score	1265	DB	3	Length	1233
Best Local	Similarity	98.0%	Pred.	No. 0				
Matches	1280	Conservative	0	Mismatches	26	Indels	0	Gaps
QY	1	ATGAAAGCGATCTTAAATCCCATTTTATCTCTTCGTATCCGTTAACCCCGCAATCTGCA	60					
Db	1	ATGAAAGCGATCTTAAATCCCATTTTATCTCTTCGTATCCGTTAACCCCGCAATCTGCA	60					
QY	61	TTGGCTCAGAGTAGCGCGAGCTGAAGCTGGAAGTGGTGAATTGCACTGCTCATGGT	120					
Db	61	TTGGCTCAGAGTAGCGCGAGCTGAAGCTGGAAGTGGTGAATTGCACTGCTCATGGT	120					
QY	121	GTGGCTCTCAACCAAGGCCACGCACTGATGCAAGATGTCAACCCCAAGCATGAGCA	180					
Db	121	GTGGCTCTCAACCAAGGCCACGCACTGATGCAAGATGTCAACCCCAAGCATGAGCA	180					
QY	181	ACCGGCGCGGTAAACCTGGGTGAGCTGACACCGCGCGTGGTGAAGTAAATCGCTATCTC	240					
Db	181	ACCGGCGCGGTAAACCTGGGTGAGCTGACACCGCGCGTGGTGAAGTAAATCGCTATCTC	240					
QY	241	GGACATTAATGCGGCTCAGCGCTCTGTGTAACCGACGATGTGCTGCTAAATGGCTGCCG	300					
Db	241	GGACATTAATGCGGCTCAGCGCTCTGTGTAACCGACGATGTGCTGCTAAATGGCTGCCG	300					
QY	301	CAGCTCTGTCAAGTTCGAGTATGTCAGACAGCGCTACCGGTAAACAGCGCA	360					
Db	301	CAGCTCTGTCAAGTTCGAGTATGTCAGACAGCGCTACCGGTAAACAGCGCA	360					
QY	361	GCTTTCGCGCGCGGAGCTGCACTGATGTGCAATAACGTAACATCCAGGAGATACG	420					
Db	361	GCTTTCGCGCGCGGAGCTGCACTGATGTGCAATAACGTAACATCCAGGAGATACG	420					
QY	421	TCCAGTCCCGATCCGTTATTTAAATCCCTCTAAACCTGGCTTGGCACTGATAAACGCG	480					
Db	421	TCCAGTCCCGATCCGTTATTTAAATCCCTCTAAACCTGGCTTGGCACTGATAAACGCG	480					
QY	481	AACGTGACTGACCGGATCTCTGAGAGGGCAGAGGGCTCAATGCTGACTTAAACCGGCAAT	540					
Db	481	AACGTGACTGACCGGATCTCTGAGAGGGCAGAGGGCTCAATGCTGACTTAAACCGGCAAT	540					
QY	541	TATCAACAGCGGCTTTCGCGAATCTGAAACGCGTCTTATTTTCGCAATCAAACTTGTGC	600					
Db	541	TATCAACAGCGGCTTTCGCGAATCTGAAACGCGTCTTATTTTCGCAATCAAACTTGTGC	600					
QY	601	CTTAAACGTGAGAAACAGACGAAAGCTGTTCATTTAACGACGATTAACATGGGAATCTC	660					
Db	601	CTTAAACGTGAGAAACAGACGAAAGCTGTTCATTTAACGACGATTAACATGGGAATCTC	660					
QY	661	AAGGTGAGCGCGCACTGTCTCATTTAAACGCGTGGTAAAGCTTCGATCAATGCTGACG	720					
Db	661	AAGGTGAGCGCGCACTGTCTCATTTAAACGCGTGGTAAAGCTTCGATCAATGCTGACG	720					
QY	721	GAGATATTTCTCTGCAACAAGCAACAGGAAATGCGGAGCGGGGTGGGAGAGATCAAC	780					
Db	721	GAGATATTTCTCTGCAACAAGCAACAGGAAATGCGGAGCGGGGTGGGAGAGATCAAC	780					
QY	781	GATTCACACAGTGGAAACACCTTGTCTAAGTTTGCAATACCGCAATTTGATTGCTACAA	840					
Db	781	GATTCACACAGTGGAAACACCTTGTCTAAGTTTGCAATACCGCAATTTGATTGCTACAA	840					
QY	841	CGACGCGCAGAGGTGGCCGAGCGCGGCAACCCGTTATTTGATTTGATCAACAGCG	900					
Db	841	CGACGCGCAGAGGTGGCCGAGCGCGGCAACCCGTTATTTGATTTGATCAACAGCG	900					
QY	901	TTGACGCGCCATCCACCGCAAAAACAGCGTATGTGTGACATTAACCACTTCAGTACTG	960					
Db	901	TTGACGCGCCATCCACCGCAAAAACAGCGTATGTGTGACATTAACCACTTCAGTACTG	960					
QY	961	TTTATTCGCGGACAGATCTAATCTTGCAATCTTCGGCGGCGCATGAGACTCACTGG	1020					
Db	961	TTTATTCGCGGACAGATCTAATCTTGCAATCTTCGGCGGCGCATGAGACTCACTGG	1020					

QY 1021 AGCTTCCCGCTCAGCCGAGTAACACGCCGAGGTGTAACTGTGTGTAAGAGCTGG 1080
DB 1021 AGCTTCCCGCTCAGCCGAGTAACACGCCGAGGTGTGTAAGAGCTGG 1080
QY 1081 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1140
DB 1081 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1140
QY 1141 CAGATCGGTGATTAACAGCCGAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1200
DB 1141 CAGATCGGTGATTAACAGCCGAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1200
QY 1201 CTGGCAGATGTGAAGAGCGAAATGCGCAGGAGTGTGTGTTGAGGTTTACGAA 1260
DB 1201 CTGGCAGATGTGAAGAGCGAAATGCGCAGGAGTGTGTGTTGAGGTTTACGAA 1260
QY 1261 ATGTGAATGAACGACGATACCGGCGTGTGATTCAGTGTGATTCATC 1306
DB 1261 ATGTGAATGAACGACGATACCGGCGTGTGATTCAGTGTGATTCATC 1306

RESULT 4

US-09-540-149A-9
; Sequence 9, Application US/09540149A
; Patent No. 6511699
; GENERAL INFORMATION:
; APPLICANT: Lee, Xinggen
; TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYLASE ACTIVITY
; FILE REFERENCE: 19603/2791
; CURRENT APPLICATION NUMBER: US/09/540,149A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/127,032
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-540-149A-9

Query Match 93.9%; Score 1228; DB 4; Length 1489;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 ATGAAGCGATCTTAATCCCATTTTATCTCTGATTCGTTAACCCGCAATCTGA 60
DB 182 ATGAAGCGATCTTAATCCCATTTTATCTCTGATTCGTTAACCCGCAATCTGA 241
QY 61 TTGCTCAGAGTGAAGCGGAGCTGAAGTGTGATTTGTCATGTGATGT 120
DB 242 TTGCTCAGAGTGAAGCGGAGCTGAAGTGTGATTTGTCATGTGATGT 301
QY 121 GTGGGTGTCAACCAAGGCGCACTGATGTGAGATGTCACCCGAGCATGAGCA 180
DB 302 GTGGGTGTCAACCAAGGCGCACTGATGTGAGATGTCACCCGAGCATGAGCA 361
QY 362 GTGGGTGTCAACCAAGGCGCACTGATGTGAGATGTCACCCGAGCATGAGCA 421
DB 421 GTGGGTGTCAACCAAGGCGCACTGATGTGAGATGTCACCCGAGCATGAGCA 481
QY 481 GTGGGTGTCAACCAAGGCGCACTGATGTGAGATGTCACCCGAGCATGAGCA 541
DB 541 GTGGGTGTCAACCAAGGCGCACTGATGTGAGATGTCACCCGAGCATGAGCA 601

QY 421 TCCAGTCCCGATCCGTTATTTAATCTCTTAAACTGTGCTTTGCCAATCTGAATAAGCG 480
DB 602 TCCAGTCCCGATCCGTTATTTAATCTCTTAAACTGTGCTTTGCCAATCTGAATAAGCG 661
QY 481 AAGGTGATGAGCGGATCTCTGAGAGGAGGAGGAGGATTTGCTGACTTTACCGGCAAT 540
DB 662 AAGGTGATGAGCGGATCTCTGAGAGGAGGAGGAGGATTTGCTGACTTTACCGGCAAT 721
QY 541 TATCAACGCGGTTTCCGCAACTGGAACGAGTGTGATTTTCCGATCAAACTGTGTC 600
DB 722 CGGCAACGCGGTTTCCGCAACTGGAACGAGTGTGATTTTCCGATCAAACTGTGTC 781
QY 601 CTTAACGTTGAGAAACAGAGCGAAAGCTGTTCATTAACGAGGATTAACATGAGAACTC 660
DB 782 CTTAACGTTGAGAAACAGAGCGAAAGCTGTTCATTAACGAGGATTAACATGAGAACTC 841
QY 661 AAGGTGAGCGGATCTCTGATTTAATCCGTTGAGGATTCGATCAATGCTGACG 720
DB 842 AAGGTGAGCGGATCTCTGATTTAATCCGTTGAGGATTCGATCAATGCTGACG 901
QY 721 GAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGGAGTGTGAGAAAGTACC 780
DB 902 GAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGGAGTGTGAGAAAGTACC 961
QY 781 GATTCAACAGGATGAAACACCTTCTAAGTTTGCATTAACGCGCAATTTGATTTGCTCAA 840
DB 962 GATTCAACAGGATGAAACACCTTCTAAGTTTGCATTAACGCGCAATTTGATTTGCTCAA 1021
QY 841 CGCAGCGGAGGTTTCCGCAACTGGAACCGGCGCAAGGATTTGATTTGATTTGATTTGAT 900
DB 1022 CGCAGCGGAGGTTTCCGCAACTGGAACCGGCGCAAGGATTTGATTTGATTTGATTTGAT 1081
QY 901 TTGAGCGGCGCATTCACAGGCAAAACAGGCGTATGATGATTAACCACTTCACTGCTG 960
DB 1082 TTGAGCGGCGCATTCACAGGCAAAACAGGCGTATGATGATTAACCACTTCACTGCTG 1141
QY 961 TTTATGCGCGGACAGATTAATCTGGAATATCTGCGGCGGCACTGAGCTTAATCTG 1020
DB 1142 TTTATGCGCGGACAGATTAATCTGGAATATCTGCGGCGGCACTGAGCTTAATCTG 1201
QY 1021 AGCTTCCCGCTCAGCCGAGTAACACGCCGAGGTGTGTAAGAGCTGG 1080
DB 1202 AGCTTCCCGCTCAGCCGAGTAACACGCCGAGGTGTGTAAGAGCTGG 1261

QY 1081 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1140
DB 1262 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1321
QY 1141 CAGATCGGTGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1200
DB 1322 CAGATCGGTGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACG 1381
QY 1201 CTGGCAGATGTGAAGAGCGAAATGCGCAGGAGTGTGTGTTGAGGTTTACGAA 1260
DB 1382 CTGGCAGATGTGAAGAGCGAAATGCGCAGGAGTGTGTGTTGAGGTTTACGAA 1441
QY 1261 ATGTGAATGAACGACGATACCGGCGTGTGATTCAGTGTGATTCATC 1300
DB 1442 ATGTGAATGAACGACGATACCGGCGTGTGATTCAGTGTGATTCATC 1481

RESULT 5

US-08-910-798-1
; Sequence 1, Application US/08910798
; Patent No. 5876997
; GENERAL INFORMATION:
; APPLICANT: KRETZ
; TITLE OF INVENTION: NOVEL PHYLASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

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STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: PHYLASE
FEATURE:
NAME/KEY:
LOCATION:
US-08-910-798-1

Query Match      88.1%; Score 1153; DB 2; Length 1272;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 26; Indels 51; Gaps 1;
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QY 541 TATCAAGCGCGTTTCGCACTGAAAGCGGTGCTTAATTTCCGCAATCAACTTTCG 600
DB 490 CGGCAAGCGCGTTTCGCACTGAAAGCGGTGCTTAATTTCCGCAATCAACTTTCG 549
QY 601 CTAAAGCTGAGAAACAGAGAGAAAGCTTTCATTAACGACGATTCACATCGGAACTC 660
DB 550 CTAAAGCTGAGAAACAGAGAGAAAGCTTTCATTAACGACGATTCACATCGGAACTC 609
QY 661 AAGTAGGCGCGACTGTGTCTCATTAACGCGGTGCGTAAAGCTTCGCAATGCTGACG 720
DB 610 AAGTAGGCGCGCAATGTCTCATTAACGCGGTGCGTAAAGCTTCGCAATGCTGACG 669
QY 721 GAATATTTCTCTGCAACAGACAGGAAATCCCGAGCCGGGGTGGGAAAGATACCC 780
DB 670 GAATATTTCTCTGCAACAGACAGGAAATCCCGAGCCGGGGTGGGAAAGATACCC 729
QY 781 GATTACACCAAGTGAACAACCTTGTAAGTTGCAATACGCGCAATTTGATTTGCTACAA 840
DB 730 GATTACACCAAGTGAACAACCTTGTAAGTTGCAATACGCGCAATTTGATTTGCTACAA 789
QY 841 CGCAGCGCAGAGGTTCGCGCAGCGCGCCGCAACCCGTTATTGATTTGATGAAGACGG 900
DB 790 CGCAGCGCAGAGGTTCGCGCAGCGCGCCGCAACCCGTTATTGATTTGATGAAGACGG 849
QY 901 TTGACGCCCATATCCACCGCAAAAACAGGCGTANAGTGATGACATTACCCACTCAAGTCTG 960
DB 850 TTGACGCCCATATCCACCGCAAAAACAGGCGTANAGTGATGACATTACCCACTCAAGTCTG 909
QY 961 TTATGCGCGGACACGATATCTAATCTGCGAATCTCGCGCGGCACTGAGCTCAACTCG 1020
DB 910 TTATGCGCGGACACGATATCTAATCTGCGAATCTCGCGCGGCACTGAGCTCAACTCG 969
QY 1021 AAGCTTCCCGGTGAGCGCGGATTAACGCGCGGAGGTGTAAGTGTGTTGAACGCTCG 1080
DB 970 AAGCTTCCCGGTGAGCGCGGATTAACGCGCGGAGGTGTAAGTGTGTTGAACGCTCG 1029
QY 1081 CGTGGGTAAGCGATTAACGCGGATGATGATGCTGCTGCTTCGCACTTACG 1140
DB 1030 CGTGGGTAAGCGATTAACGCGGATGATGATGCTGCTGCTTCGCACTTACG 1089
QY 1141 CAGATGCGGATTAAGCGCGGCTGCTGATTAATACGCGCGCGGAGGTGAACTGACG 1200
DB 1090 CAGATGCGGATTAAGCGCGGCTGCTGATTAATACGCGCGCGGAGGTGAACTGACG 1149
QY 1201 CTGCGAGATGTGAAGAGCAATGCGCAGGCGATGTGTTGCGACGTTTACGAA 1260
DB 1150 CTGCGAGATGTGAAGAGCAATGCGCAGGCGATGTGTTGCGACGTTTACGAA 1209
QY 1261 ATGCTGAATGAACACGCAATCCGGGCTGCACTTTAAGATTCATC 1306
DB 1210 ATGCTGAATGAACACGCAATCCGGGCTGCACTTTAAGATTCATC 1255

RESULT 6
US-09-489-039A-341
Sequence 341, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIORITY FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 341
LENGTH: 1266
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-341
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Query Match	5.1%*	Score 66.2	DB 4	Length 1266
Best Local Similarity	49.2%*	Pred. No. 7.5e-12		
Matches 204	Conservative 0	Mismatches 208	Indels 3	Gaps 1
QY	86	AGCTGAAAGTGTGTGATTTGTGATGTCATGTGTGTGCTCTCC--AAACCAAGGCCA	142	
Db	113	AGCTGACGACAGTGTCTGATTCATGTAGCCCTCAACCTGCTGTGCGCTTGGCCATTAACG	172	
QY	143	CGCAACAGTATGCAGGATATGTCACCCCAAGCGATGGCCAACTGGCGGGTAAACTGGGTG	202	
Db	173	GCAAGCTGTCTGAAACATGTCCACCCGCAAGGCTTGGCCGAGTGGATGTGCCGGCGGCC	232	
QY	203	AGCTGACACCGCGCGGTGTGAGCTTAATGCGCTATCTTGAACATTACTGGCGTCAAGCTC	262	
Db	233	AGCTGACACCAAAAGGCGGTGTGCTGAGGATGTATATGAGCACTAATATGCGCGAATGGC	292	
QY	263	TGTGATGCCGACGAGTGTGTGCTTAAATGTGCTGTCCCGGCACTGTGTGATGAGTGGCGATTA	322	
Db	293	TGGGCGACGACAAAGTGTGTGACACGCGCGAGTGTCCCGGAAAACGGGTTTATGTGCTT	352	
QY	323	TTGTGTATGTGACAGCGCGTACCCGCTAAACAGCGGAAAGCCTTGGCGCGCGCTGACAC	382	
Db	353	ACGCTTAACAGCTGTGACGACCGCTGACCGCGCACTTTTATTAACCGCGCGGTTC	412	
QY	383	CTGACTGTGCAATTAACCTTAATACCCAGGCGAGTACGTCCAGTCCCATTCCTTATTTA	442	
Db	413	CGGGGTGGGGATCCCGGTGTGATCAACGCTCAATATGAGGACCAATGACCCGACCTTCA	472	
QY	443	ATCCTCTTAAAACTGGCGCTTTGCCAATCGATTAACGCCAAGTGTACTGACGCGAT	497	
Db	473	ACCGGTTATTATTAACGACGACACTCCCGGGGTTTGGGAAAGAGCGCTGACAGGGAT	527	
RESULT 7				
US-09-621-976-15639/c				
Sequence 15639, Application US/09621976				
Patent No. 6639063				
GENERAL INFORMATION:				
APPLICANT: Dumas MLine Edwards, J.B.				
APPLICANT: Jobert, S.				
APPLICANT: Giordano, J.Y.				
TITLE OF INVENTION: ESTs and Encoded Human Proteins.				
FILE REFERENCE: GENSET.054PR2				
CURRENT APPLICATION NUMBER: US/09/621.976				
CURRENT FILING DATE: 2000-07-21				
NUMBER OF SEQ ID NOS: 19335				
SOFTWARE: Patent.pm				
SEQ ID NO 15639				
LENGTH: 505				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-621-976-15639				
Query Match: 3.0% Score 39.8; DB 4; Length 505;				
Best Local Similarity 11.7% Pred. No. 0.0036;				
Matches 43; Conservative 172; Mismatches 144; Indels 10; Gaps 1				
QY	73	GAGCCGAGCTGAAAGCTGAAAAGTGTGTGATTTGTCACTCGTCATGTTGTGCGTCTCA	132	
Db	359	GGSYCGMTSYTSGSKMTGRKGSMTYRKRMWTYSXGMMWTYSXCTKTGKYTGKSKXTWT	300	
QY	133	ACCAAGGCCACCGCACTGATGTGAGGATGTCAACCCAGACGATGGCCAACTGCGCGGTA	192	
Db	299	CTSMKTYMMNMSGCAASWKSWSKASWYSWMACTCMMSASAYARSMTGARRSMRAGAG	240	
QY	193	AAACTGGGTGAGCTACACCGCGCGGTGTGAGCTAATGCGCTATCTGCGACATTACTGG	252	
Db	229	WWRARGRKKRARGKSKMSRWSKYSWMSAGKALMCRPMWSCRMYSYCMGSKCMSCRGT	180	
QY	253	CGTACGCGTGTGTGAGCCGACGAGATTGTCTGCTTAATATGTGGTGTCCCGGAGTGTGTAG	312	
Db	179	CAKMKRIVATRYAKRYASMG-----KIMGCKWCTYAKARNTGYTRSRSTGSGTG	130	

```

OY 311 GTCGGGATTTGTCGATGTCGACGAGCTAACCCGTTAAACAGGCGAAGCTTCCGCCCC 372
Db 129 KTRRRKRYTHMKTMWMSWCTRYGAAATYGMSPAYRTMTASMSACMCRMMKMSNMW 70
OY 373 GGGCTGCGACCTGATGTGTGCAATTAACGATACATACCAGCAGATACGTCCAGTCCCAT 432
Db 69 MCGMSRKYCWMSGKWCYSCCGYCCSACFMICYMTIRMTMSWYSRRKSRMSMSAY 10
OY 433 CCGTATTT 441
Db 9 RYSSKRTKT 1

RESULT 8
US-09-710-794-4/C
Sequence 4, Application US/09710794
Patent No. 6573069
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
TITLE OF INVENTION: NOVEL CRIB PROTEIN ZMSL
FILE REFERENCE: 99-76
CURRENT APPLICATION NUMBER: US/09/710,794
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164,685
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2868
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (173)...(1219)
US-09-710-794-4

Query Match 2.8%; Score 36.6; DB 4; Length 2868;
Best Local Similarity 52.3%; Pred.No.0.13;
Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0

OY 128 CTCGACACGAGCGCAGCGAATCTGATGACAGATGTCAACCCAGACGATGGCCAACTGGCC 187
Db 353 CTCCTCTCCCTGCTCTGTGATGAGAGAGAGGTGTCCCAAAGAGCTCCCAAGCCCGCC 294
OY 188 CGGTAATACGTGGTGTAGGTGACACCGCGCGGTGTGAGCTAATCGCTAATCTCGACAT 247
Db 293 CCACATGACATGGTGTGGGGAAGTCAACCCAGCGGACATGATCACTCGGCTGTAGGT 234
OY 248 ACTGCGCTCAGCGTCTGTGTAAGCCAGCGATTGCTG 282
Db 233 CCGCACGTGAGCGGCGCTTGAGTTCAAGAGCTG 199

RESULT 9
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765

```

TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.6%; Score 34.4; DB 3; Length 4403765;
Best Local Similarity 52.9%; Pred. No. 50;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 262 CTGGAGCCGACGAGATTGCTGCTTAATGTGCTGCCGCGAGTCTGTGTCAGGTGCGCAT 321
DB 3709961 CAGGTGCGCCCCGCGACTGCTGGAATCCCTGCTGCGGAGCTGACTGACGCCAAATC 3710020
QY 322 ATTGCTGATGTGACGACGAGCCGTAAACAGGCGAAGCCTTGCCCGCGGCTGACA 381
DB 3710021 GTCCGCGAAGCCGCGGAGTGAACCGGTTCAAAAGCGAAGCCGCTTGCCCATGCC 3710080
QY 382 CCTGACTGTGAATACCGT 401
DB 3710081 GAGTGGCTCCATCCCGT 3710100

RESULT 10
US-09-103-840A-1

Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.6%; Score 34.4; DB 3; Length 4411529;
Best Local Similarity 52.9%; Pred. No. 50;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 262 CTGGAGCCGACGAGATTGCTGCTTAATGTGCTGCCGCGAGTCTGTGTCAGGTGCGCAT 321
DB 3712396 CAGGTGCGCCCCGCGACTGCTGGAATCCCTGCTGCGGAGCTGACTGACGCCAAATC 3712455
QY 322 ATTGCTGATGTGACGACGAGCCGTAAACAGGCGAAGCCTTGCCCGCGGCTGACA 381
DB 3712456 GTCCGCGAAGCCGCGGAGTGAACCGGTTCAAAAGCGAAGCCGCTTGCCCATGCC 3712515
QY 382 CCTGACTGTGAATACCGT 401
DB 3712516 GAGTGGCTCCATCCCGT 3712535

RESULT 11
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.6%; Score 34.2; DB 3; Length 4403765;
Best Local Similarity 52.4%; Pred. No. 56;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 176 GCGCACTGCGCGGTAATACTGGGTGAGCTGACACCGCGGCTGAGTATGCGCT 235
DB 3381125 GCGCGCGGTGACGACCACTCCGTTGACATATACCACTGACGCGACCGCTCGACC 3381066
QY 236 ATCTGACATTAATGCGCTGACCGTCTGTGATGCGGAGCGAGTCTGCTTAATGTGCT 295
DB 3381065 GCTCCGCGCTTGTGCGCGACGACACTGTGCGGTGCGTTCGCTGACCGTG 3381006
QY 296 GCGCGAGTGTGTCAAGTCCG 318
DB 3381005 CGCGGACGCTGCGGTGCG 3380983

RESULT 12

US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.6%; Score 34.2; DB 3; Length 4411529;
Best Local Similarity 52.4%; Pred. No. 56;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 176 GCGCACTGCGCGGTAATACTGGGTGAGCTGACACCGCGGCTGAGTATGCGCT 235
DB 3385432 GCGCGCGGTGACGACCACTCCGTTGACATATACCACTGACGCGACCGCTCGACC 3385373
QY 236 ATCTGACATTAATGCGCTGACCGTCTGTGATGCGGAGCGAGTCTGCTTAATGTGCT 295
DB 3385372 GCTCCGCGCTTGTGCGCGACGACACTGTGCGGTGCGTTCGCTGACCGTG 3385313
QY 296 GCGCGAGTGTGTCAAGTCCG 318
DB 3385312 CGCGGACGCTGCGGTGCG 3385290

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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match          2.6%   Score 33.8; DB 4; Length 399;
Best Local Similarity 10.6%; Pred. No. 0.34; Mismatches 153; Indels 0; Gaps 0
Matches 38; Conservative 156;

QY      457 GGCCTTGGCAACTGATATACCGAAGCTGACGCCGATCTCTCGAGAAGGCGAGAGG 516
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      10 KCAKAPAAATPRAVWGMVTRGSKSWRAKMSMKRRRBRRAAMVMWSMCMMKSKSMMNS 69
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      517 TCAATTGTGCACTTAACCGGGCATTTAACCAACGCGCTTGCCGAACGTGAACGGGTGCTT 576
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      70 WGVNTAKMGRABASNAGTSMWTMTMRKRYYTKRKACTTKPRASMGKKGMAMAYATA 129
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      577 AATTTTCGCAATCAAATCTGTGCTTAAACGTGAAGAACGACGAACTGTTCATTA 636
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      130 KMVYAMERTAKRYAMNMKSRSMBRPBAYAMYIMARIVMGMAISCYRAYVASG 189
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      637 AGCAGGCACTTCCATCGAAGCTGAAGGTGACGCCGACTGTGTCTCATTAACCGGTGCG 696
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      190 MYTMMMYTMRMKMYTSAGMSMKRTKRCASYCMSYSYCMGAXMMYMKTSRWNYVS 249
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      697 GTAAGCTTCGATCAATCTGAACGAGATATTTCTCTGCAACAGCACAGGAAATGCCG 756
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      250 SYCTCYRRSCCCMSMSCYWKTYVRSWYCASCYISYTKXASCOMMCCMKWRMMAMMY 309
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      757 GAGCGCGGGTGGGAGAGATCACCGATTCACACAGAGTGAACAACCTTGCTAAGTTG 813
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      310 MMATTCCKTSMRYRRCYSIAKMRMRMMCAYMMMTGCMWMWCWTGGCTATTTG 366
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-08-680-326-116/c
Sequence 116, Application US/08680326
Patent No. 5925733
GENERAL INFORMATION:
APPLICANT: ROSE, TIMOTHY M.
APPLICANT: BOSCH, MARINX
APPLICANT: STRAND, KURT
APPLICANT: TODARO, GEORGE J.
TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,326
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schliff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29938-20001.00
TELECOMMUNICATION INFORMATION:

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Tue May 4 07:05:31 2004

us-09-866-379d-9.rni

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TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 116
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2511
US-08-680-326-116

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Query Match          2.5%   Score 33; DB 2; Length 2511;
Best Local Similarity 49.7%   Pred. No 1.9;
Matches      84; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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QY	519	AATGGCTACCTTTACCGGGCACTTTCAAACGGCGCTTTGGCGAACCTGGAAACGGGGTCTTAA	578
Db	1198	CCCGATCTGTGGGCGCCGTCGTACGTAACCTCAACGGGTGGGATCTTGGCCACGCTTGGCTA	1139
QY	579	TTTTCCGCACTCAACTTTCGCTTAAACGTGAGAAACAGACGAAACG	627
Db	1138	TTTCCGAGATCTCAACATGGGCTTGAAACCGTAGCAAGATCCACTAAC	1090

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Tue May 4 07:05:30 2004

US-09-866-379d-7.rmpb

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 21:42:28 ; Search time 771.893 Seconds
(without alignments)
1140.289 Million cell updates/sec

Title: US-09-866-379D-7
Perfect score: 1901
Sequence: 1 taagagcagaacatgctg.....gtaattgacgacatcgatcg 1901

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1900	99.9	1901	9	US-09-866-379-7
2	1900	99.9	1901	15	US-10-156-660-3
3	1898.4	99.9	1901	9	US-09-866-379-5
4	1898.4	99.9	1901	9	US-09-866-379-9
5	1895.2	99.7	1901	9	US-09-866-379-6
6	1440.2	75.8	1486	16	US-10-284-962-4
7	1397.4	73.5	1489	15	US-10-266-041-9
8	1397.4	73.5	1489	16	US-10-284-962-1
9	1398	68.3	1289	13	US-10-282-122A-167
10	1287.8	67.7	1323	9	US-09-777-566A-1
11	1287.8	67.7	1323	9	US-09-866-379-1
12	1287.8	67.7	1323	15	US-10-034-985-1
13	1287.8	67.7	1323	16	US-10-430-356-1
14	1263.8	66.5	1308	15	US-10-156-660-1

15	669.6	35.2	1281	15	US-10-334-672-4	Sequence 4, Appli
16	669.6	35.2	1281	15	US-10-334-671-4	Sequence 4, Appli
17	466	24.5	466	13	US-10-282-122A-3181	Sequence 3, Appli
18	299.4	15.7	2181	13	US-10-282-122A-20324	Sequence 20324, A
19	229.2	12.1	1326	13	US-10-282-122A-41608	Sequence 41608, A
20	225.2	11.8	1325	15	US-10-021-723A-3	Sequence 3, Appli
21	222.4	11.7	254	16	US-10-317-444-302	Sequence 302, App
22	222.4	11.7	254	16	US-10-317-444-302	Sequence 302, App
23	222.4	11.7	254	16	US-10-317-444-303	Sequence 304, App
24	222.4	11.7	254	16	US-10-317-444-304	Sequence 304, App
25	222	11.7	1325	15	US-10-021-723A-1	Sequence 1, Appli
26	211.4	11.1	1325	15	US-10-021-723A-11	Sequence 11, Appli
27	158	8.3	1431	15	US-10-021-723A-9	Sequence 9, Appli
28	111.4	5.9	1282	13	US-10-282-122A-19198	Sequence 19198, A
29	107.6	5.7	2160	13	US-10-282-122A-22963	Sequence 22963, A
30	101.4	5.3	2160	13	US-10-282-122A-19913	Sequence 39913, A
31	100.2	5.3	2199	13	US-10-282-122A-20408	Sequence 20408, A
32	73	3.8	1230	15	US-10-021-723A-7	Sequence 7, Appli
33	68	3.6	2232	13	US-10-282-122A-13362	Sequence 13362, A
34	64.8	3.4	1266	15	US-10-021-723A-5	Sequence 5, Appli
35	62.4	3.3	2202	13	US-10-282-122A-13620	Sequence 13620, A
36	61.4	3.2	2238	13	US-10-282-122A-13655	Sequence 13655, A
37	58.8	3.1	2220	13	US-10-282-122A-12931	Sequence 12931, A
38	56.8	3.0	11710	15	US-10-240-689-40	Sequence 40, Appli
39	55.2	2.9	2337	9	US-09-934-899-7	Sequence 7, Appli
40	55.2	2.9	2337	9	US-09-934-868-27	Sequence 27, Appli
41	55.2	2.9	2337	15	US-10-353-457-7	Sequence 7, Appli
42	55.2	2.9	2337	15	US-10-353-456-7	Sequence 7, Appli
43	51.4	2.7	5738	8	US-08-781-986A-84	Sequence 84, Appli
44	51.4	2.7	5738	13	US-10-329-624-84	Sequence 84, Appli
45	46	2.4	2208	13	US-10-282-122A-13591	Sequence 13591, A

ALIGNMENTS

US-09-866-379-7

Sequence 7, Application US/09866379

Parent No. US20020136754A1

GENERAL INFORMATION: CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: KREITZ, Keith

APPLICANT: BARTON, Nelson

APPLICANT: GARRETT, James

APPLICANT: O'DONOGHUE, Eileen

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.1

SEQ ID NO 7

LENGTH: 1901

TYPE: DNA

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(1901)

OTHER INFORMATION: n is any nucleotide

US-09-866-379-7

Query Match 99.9%; Score 1900; DB 9; Length 1901;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TAAAGACAGAAAACAATGATGATTTTACTTGTGTCGCGCATTTGTGATGTCG 60
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DB 61 CTCCTCAACCCCTTGTTGTTGATGTCGACCCGCTGTAAGAAAGTTAACGACGTC 120
QY 121 TGAAGCGCGCATAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 180
DB 121 TGAAGCGCGCATAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 180
QY 181 CATATGATGAAAGCGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAA 240
DB 181 CATATGATGAAAGCGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAA 240
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DB 301 TCATGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
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DB 721 CGGCGATCGGAAAGCGGCTTCGGAACGTCGGAACGTCGGAACGTCGGAAC 780
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DB 1081 GACAGCGTTGACGCGCCATCCACCGCAAAAACAGCGTATGTCGATTAACCACTTC 1140
QY 1141 AGTGTGTTTACCGCGGACAGATCTAATCTGCAAAATCTGCGCGCGCATGAGCT 1200
DB 1141 AGTGTGTTTACCGCGGACAGATCTAATCTGCAAAATCTGCGCGCGCATGAGCT 1200
QY 1201 CAATGAGACGTCCTCCGTCAGCGGATTAACGCGCGCAAGTCGATGATGTTGA 1260
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DB 1261 AGCTGCGCTGCGCTTAACCGCAATTAACGCAAGTCAGTTTCGCTGCTTCAAG 1320
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DB 1321 TTTACAGAGATGCGTATTAACGCGCTGTCATTAATACGCGCGCGAGAGTGAA 1380
QY 1381 ACTGACCTTCGCGAGATGTAAGAGCGAATGCGAGGAGGAGTGTGTCGTCGAGTTT 1440
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QY 1441 TACGCAAAATCGTATGTAAGACAGCATACCGCGTCAGTTGTAATGATTAAGAA 1500
DB 1441 TACGCAAAATCGTATGTAAGACAGCATACCGCGTCAGTTGTAATGATTAAGAA 1500
QY 1501 CATTAATTAATCTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1560
DB 1501 CATTAATTAATCTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1560
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QY 1681 TGAAGTAAGCGCTTAAATTAATGAAGCGCTGCTGTCAGAGCGTCGATGAACA 1740
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QY 1741 CCTCTTGGCGGTGTTCAAGCCAAAACGCGCAACGAGGCTGTCGCAACAGAGC 1800
DB 1741 CCTCTTGGCGGTGTTCAAGCCAAAACGCGCAACGAGGCTGTCGCAACAGAGC 1800
QY 1801 CCAAGACCGCGGATTAACCAACCGCAAGTCGAGCGGAGTATGCAATCAACATG 1860
DB 1801 CCAAGACCGCGGATTAACCAACCGCAAGTCGAGCGGAGTATGCAATCAACATG 1860
QY 1861 AATGTCGTCGCGCATTCAGTAATTAATGAGCATCGATG 1901
DB 1861 AATGTCGTCGCGCATTCAGTAATTAATGAGCATCGATG 1901

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RESULT 2
 US-10-156-660-3
 ; Sequence 3, Application US/10156660
 ; Publication No. US20030103958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Short, Jay M.
 ; APPLICANT: Kretz, Keith
 ; APPLICANT: Gray, Kevin A.
 ; APPLICANT: Barton, Nelson R.
 ; APPLICANT: Garrett, James B.
 ; APPLICANT: O'Donoghue, Eileen
 ; APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US/10/156,660
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 403
OTHER INFORMATION: n = A,T,C or G
US-10-156-660-3

Query Match 99.9%; Score 1900; DB 15; Length 1901;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TAAGAGCAGAAACATGTTGTTTACTTGTGTTGTCGCGCATTTTGTGATGTTCG 60
61 CTCACACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
61 CTCACACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
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121 TGATGCGGCGATTAGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCAT 180
181 CATATCGATGAAGAGATGATTAATCCATTTTATCTTCTGATGTCGTTAACCCGCA 240
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241 ATCTGATTCGCTGAGATGAGCCGGAAGCTGAAGTGAAGTGAAGTGAAGTGAAGT 300
241 ATCTGATTCGCTGAGATGAGCCGGAAGCTGAAGTGAAGTGAAGTGAAGTGAAGT 300
301 TCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360
301 TCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360
361 ATGCGCAACCTGCGCGGTAAACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 420
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421 CATATTCGCACTTACCAAGCCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
421 CATATTCGCACTTACCAAGCCGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
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481 CTGCGCGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 540
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541 AGCGAAGCTTTCGCGCGGCTGCGCATGCTGATGCTGATGCTGATGCTGATGCTG 600
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661 TAACCGGAACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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901 GCTGACGAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGGCTGCGGAGAG 960
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1021 GCTAACAAGCAAGCGGAGGTTCCGCGACGCGCGCACCCGCTTATTAATTAATCA 1080
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1081 GACAGGTTGAGCGCCCATCAACCGCAAAACAGGCGTATGCTGATGCTGCTGCTG 1140
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1201 CAATCGAAGCTTCCGCGTCAACCGGATTAACAGCGCGCGGAGTGAATGCTGTTGA 1260
1261 ACCTGCGCTCGGCTAAGCATTAACGCGCATGATTAAGTGTGCTGCTGCTGCTG 1320
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1441 ACTGACCTGCGAGATGTTGAAGAGCGAATGCGAGGCTGCTGCTGCTGCTGCTG 1500
1441 ACTGACCTGCGAGATGTTGAAGAGCGAATGCGAGGCTGCTGCTGCTGCTGCTG 1500
1501 CATTCAGTTAAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1501 CATTCAGTTAAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
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Db 1621 TATAACCGTAATAGTATAGCCCTAAGTAAAGCGGTGCGGCGCTTAAATACACCAAT 1680
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Db 1741 CCTCTTTGGGCGGTTCAGAGCCAAAACGCGCAACGAGAGCTGTGCGCAAGAAAGCGC 1800
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Db 1801 CCAAGACCGCGGATCATCTACCGCGAGCATCGCGCGCGGTATGCAATACCAAGATCGT 1860
QY 1861 AATGTCGTTCGCCCATTCAGTAATTAGAGCATCGCATCG 1901
Db 1861 AATGTCGTTCGCCCATTCAGTAATTAGAGCATCGCATCG 1901

RESULT 3

US-09-866-379-5
Sequence 5, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYLASES AND USES THEREOF
FILE REFERENCE: DIVER370-7
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 02/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1901)
OTHER INFORMATION: n is any nucleotide
US-09-866-379-5

Query March 99.9%; Score 1898.4; DB 9; Length 1901;
Best local similarity 99.9%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TAAGAGCAGAAACAATGTGTATTTAATTGTTGTTCTGCGCATTTTGTGATGTGTCG 60
Db 1 TAAGAGCAGAAACAATGTGTATTTAATTGTTGTTCTGCGCATTTTGTGATGTGTCG 60
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Db 61 CTCTCCACCTTGTGTGTATGTGCTGAGCCGCGCTGAAAAATTAAACGTAAGGCC 120
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Db 121 TGATGCGCGCATTAAGCATCGCATCAGGCAATCAATAATGTCAATATGAAAGCGGAAA 180

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Db 481 CTGCGCGAGTCTGTGATCAGTCTGAGTATTTCTGATGTCAGACGCGTAAAC 540
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Qy 1621 TATAACCTGATATGATTAAGCGCTAAGCTGTAAGGCGTGGCGGCTTATACCAACAT 1680
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Qy 1681 TGAGGATAGCCCTTTATATATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 TGAGGATAGCCCTTTATATATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
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Db 1741 CCTCTTGGCGGTGTTCAGACCAAAAGCGGCAACGAGAGCTGTGTCACAAAGCC 1800
Qy 1801 CCAGCAGCGCGCATCACTCAACCGCAGCATCGGCGGCTGATCAACATCAACAGATCGT 1860
Db 1801 CCAGCAGCGCGCATCACTCAACCGCAGCATCGGCGGCTGATCAACATCAACAGATCGT 1860
Qy 1861 AATGCTGTTGCCCATTCAGTAATTAACGATCCGATCG 1901
Db 1861 AATGCTGTTGCCCATTCAGTAATTAACGATCCGATCG 1901

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/ LENGTH: 1901
/ TYPE: DNA
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(1901)
/ OTHER INFORMATION: n is any nucleotide
US-09-866-379-9

Query Match          99.9%; Score 1898.4; DB 9; Length 1901;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TAAAGAGCAAAACAATGTGTATTTACTTGTGTGTCGCGCATTTTGTGATGTGTCG 60
Db 1 TAAAGAGCAAAACAATGTGTATTTACTTGTGTGTCGCGCATTTTGTGATGTGTCG 60
Qy 61 CTCTCAGCCCTGTGTGTGTATGCTGAGCCGCGCTGAAAGTTAAAGAAAGTAAAGAGCC 120
Db 61 CTCTCAGCCCTGTGTGTGTATGCTGAGCCGCGCTGAAAGTTAAAGAAAGTAAAGAGCC 120
Qy 121 TGAATGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Db 121 TGAATGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Qy 181 CATATGATGAAAGCAATCTTAATCCATTTTATCTCTGATTCGCTTAACCCGCA 240
Db 181 CATATGATGAAAGCAATCTTAATCCATTTTATCTCTGATTCGCTTAACCCGCA 240
Qy 241 ATCTGATTCGCTCAGAGTGAAGCCGAGTGAAGCTGAAAGTGTGTGATTTGATGTCG 300
Db 241 ATCTGATTCGCTCAGAGTGAAGCCGAGTGAAGCTGAAAGTGTGTGATTTGATGTCG 300
Qy 301 TCAATGTGTGCTGCTTCCCAACCAAGCCGCACTGAATGATGATGATGATGATGATGATG 360
Db 301 TCAATGTGTGCTGCTTCCCAACCAAGCCGCACTGAATGATGATGATGATGATGATGATG 360
Qy 361 ATGAGCAACCTGAGCGGTAAATCTGGGTTGGCTGACACCGCGAGGTGTGATGATGCT 420
Db 361 ATGAGCAACCTGAGCGGTAAATCTGGGTTGGCTGACACCGCGAGGTGTGATGATGCT 420
Qy 421 CTATCTCGACATTAACCAAGCCGATGCTGTGATGCTGATGCTGATGCTGATGCTGATGCT 480
Db 421 CTATCTCGACATTAACCAAGCCGATGCTGTGATGCTGATGCTGATGCTGATGCTGATGCT 480
Qy 481 CTGCGCGCAGTGTGCTGAGTGCAGATTAATGCTGATGCTGATGCTGATGCTGATGCTG 540
Db 481 CTGCGCGCAGTGTGCTGAGTGCAGATTAATGCTGATGCTGATGCTGATGCTGATGCTG 540
Qy 541 AGGCGAAGCCTTGGCGCGCGCTGAGCCTGATGCTGATGCTGATGCTGATGCTGATGCT 600
Db 541 AGGCGAAGCCTTGGCGCGCGCTGAGCCTGATGCTGATGCTGATGCTGATGCTGATGCT 600
Qy 601 AGATAGCTCAGTCCGATCCGATTTAATCTCTTAATACTGAGGCTGTGCAATGGA 660
Db 601 AGATAGCTCAGTCCGATCCGATTTAATCTCTTAATACTGAGGCTGTGCAATGGA 660
Qy 661 TAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
Db 661 TAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
Qy 721 CCGGCAATCGGCAAAAGCGCTTTCGCAACTGAAACGGGCTTAATTTCCGAAATCAA 780
Db 721 CCGGCAATCGGCAAAAGCGCTTTCGCAACTGAAACGGGCTTAATTTCCGAAATCAA 780
Qy 781 CTGTGCTTAAAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 840
Db 781 CTGTGCTTAAAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 840
Qy 841 GGAATCAAGTGAAGCGCGCAATGTCTCAATTAACCGGTGAGTGAAGTGAAGTGAAGTGA 900
Db 841 GGAATCAAGTGAAGCGCGCAATGTCTCAATTAACCGGTGAGTGAAGTGAAGTGAAGTGA 900

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RESULT 4
US-09-866-379-9
Sequence 9, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, Eileen
APPLICANT: O'DONOGHUE, Eileen
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1998-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9

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QY	90	GC	GACGAGCGAGATTTTCTCTCTGCAACAACACACAGGAAATGCGAGCCGGGTGGGAG	960
Dp	901	GC	TGAACGGAGATTTTCTCTCTGCAACAACACAGGAAATGCCGAGCCGGGTGGGAG	960
QY	961	GAT	CACCGATTCACACACAGTGAACA	1020
Dp	961	GAT	CACCGATTCACACACAGTGAACA	1020
QY	1021	GCT	ACAACGACGCGACAGGTTGGCCGCGACGCCGATTAATGATTTGATCAA	1080
Dp	1021	GCT	ACAACGACGCGACAGGTTGGCCGCGACGCCGATTAATGATTTGATCAA	1080
QY	1081	GAC	AGCGGTTGACGCCCCATTCACCGCAAAAACAAGCGATGCGATTAACCACTTC	1140
Dp	1081	GAC	AGCGGTTGACGCCCCATTCACCGCAAAAACAAGCGATGCGATTAACCACTTC	1140
QY	1141	AGT	CGTGTATTAATGCGCGACACATCTAATCTGGCAATCTCGCGCGACATGAGCT	1200
Dp	1141	AGT	CGTGTATTAATGCGCGACACATCTAATCTGGCAATCTCGCGCGACATGAGCT	1200
QY	1201	CA	ACTGACGCTTCCCGGTGAGCGGATTAACAGCCCGCAGGTGAACTGTTTGA	1260
Dp	1201	CA	ACTGACGCTTCCCGGTGAGCGGATTAACAGCCCGCAGGTGAACTGTTTGA	1260
QY	1261	AC	GTGCGTGGCTTAAGCATTAACAGCAGTGAATCAGTTGGCTGCTTCCAGAC	1320
Dp	1261	AC	GTGCGTGGCTTAAGCATTAACAGCAGTGAATCAGTTGGCTGCTTCCAGAC	1320
QY	1321	TTT	CACAGATGCGTATTAACAGCCGCGTGTATTAATACGCCGCCCGAGAGGTAA	1380
Dp	1321	TTT	CACAGATGCGTATTAACAGCCGCGTGTATTAATACGCCGCCCGAGAGGTAA	1380
QY	1381	ACT	GACCCCTGCGAGATGTGAAGAAGGAAATGGCGAGGCACTGTTGGTGGCAGTTT	1440
Dp	1381	ACT	GACCCCTGCGAGATGTGAAGAAGGAAATGGCGAGGCACTGTTGGTGGCAGTTT	1440
QY	1441	TAC	CAATCGTGAATGAACAGCATACCGCGGTGCACTTGTGATGAATTAATAAAG	1500
Dp	1441	TAC	CAATCGTGAATGAACAGCATACCGCGGTGCACTTGTGATGAATTAATAAAG	1500
QY	1501	CAT	CACTTAACCGTGAATGCTGTAAGCTGAAGCTGAAGAAGCAACGATTAATGCTGA	1560
Dp	1501	CAT	CACTTAACCGTGAATGCTGTAAGCTGAAGCTGAAGAAGCAACGATTAATGCTGA	1560
QY	1561	CCG	AAAAAGCGTTCACAGCCGACATCCGGCCACTTTCAGTTTCTCTTCTCGAGTAA	1620
Dp	1561	CCG	AAAAAGCGTTCACAGCCGACATCCGGCCACTTTCAGTTTCTCTTCTCGAGTAA	1620
QY	1621	TAT	TACCGTGAATGATTAACCGTGAATGATTAACCGTGAATGATTAACCGTGAAT	1680
Dp	1621	TAT	TACCGTGAATGATTAACCGTGAATGATTAACCGTGAATGATTAACCGTGAAT	1680
QY	1681	TGA	GATTAAGCGCTTATTAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
Dp	1681	TGA	GATTAAGCGCTTATTAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
QY	1741	CCT	CTTTGGCGGTGTTCAAGCAAAACGCGCAACAGCGCTGGTGGCCAAAGAGCC	1800
Dp	1741	CCT	CTTTGGCGGTGTTCAAGCAAAACGCGCAACAGCGCTGGTGGCCAAAGAGCC	1800
QY	1801	CCA	GACCGCGGCTCACTACCGCGCAGCATCCGCGCGGTATGACAAATCAACAGATGT	1860
Dp	1801	CCA	GACCGCGGCTCACTACCGCGCAGCATCCGCGCGGTATGACAAATCAACAGATGT	1860
QY	1861	AAT	GATGCTGTTGCCCATTCACGATTAATGAGCATCCGATCG	1901
Dp	1861	AAT	GATGCTGTTGCCCATTCACGATTAATGAGCATCCGATCG	1901

```

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIORITY APPLICATION NUMBER: US 09/580,515
PRIORITY FILING DATE: 2000-05-25
PRIORITY APPLICATION NUMBER: US 09/318,528
PRIORITY FILING DATE: 1999-05-25
PRIORITY APPLICATION NUMBER: US 09/291,931
PRIORITY FILING DATE: 1998-04-13
PRIORITY APPLICATION NUMBER: US 09/259,214
PRIORITY FILING DATE: 1998-03-01
PRIORITY APPLICATION NUMBER: US 09/910,738
PRIORITY FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1..(1901)
OTHER INFORMATION: n is any nucleotide
US-09-866-379-6

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Query Match	99.7%	Score 1895.2	DB 9	Length 1901				
Best Local Similarity	99.8%	Pred. No. 0						
Matches 1898	Conservative	0	Mismatches 3	Indels 0	Gaps 0			
QY	1	TAAGAGAGAAAA	CAATGTGTATTA	CTTTGGTTCGTGGCA	TTTTGTGATGTTTCG	60		
Db	1	TAAAGAGAGAAAA	CAATGTGTATTA	CTTTGGTTCGTGGCA	TTTTGTGATGTTTCG	60		
QY	61	CTTTCACCC	TTGTGTGTA	TGGCTGACCCCGGTCTG	AAAAAGTTAACGAAC	GTAAAGCC	120	
Db	61	CTCTCCACCC	TTGTGTGTA	TGGCTGACCCCGGTCTG	AAAAAGTTAACGAAC	GTAAAGCC	120	
QY	121	TGATGGCGGCGA	TTAGCATGCGATCAGGCA	TCATATA	TGACATATG	ATGAAAAAGGAGAA	180	
Db	121	TGATGGCGGCGA	TTAGCATGCGATCAGGCA	TCATATA	TGACATATG	ATGAAAAAGGAGAA	180	
QY	181	CATATCATG	AAAGCATCTTA	ATCCATTTT	ATCTTCTG	ATTCGGTTAACCCGCA	240	
Db	181	CATATCATG	AAAGCATCTTA	ATCCATTTT	ATCTTCTG	ATTCGGTTAACCCGCA	240	
QY	241	ATCTGCAT	TCGCTCAGAGT	AGCCGGAGCTGA	AGCTGGA	AAAGTGTGGTATGTCA	300	
Db	241	ATCTGCAT	TCGCTCAGAGT	AGCCGGAGCTGA	AGCTGGA	AAAGTGTGGTATGTCA	300	
QY	301	TCATGTGTGGGT	GTGTCCAA	CCAGGCCA	CGCAATG	ATGACAGAT	TCACCCGAGCGC	360
Db	301	TCATGTGTGGGT	GTGTCCAA	CCAGGCCA	CGCAATG	ATGACAGAT	TCACCCGAGCGC	360
QY	361	ATGGCAAC	CTGGCCG	GTAAACT	GGTGTGGCTGA	CACCGCGNG	TGTGAGCTAATGCG	420
Db	361	ATGGCAAC	CTGGCCG	GTAAACT	GGTGTGGCTGA	CACCGCGNG	TGTGAGCTAATGCG	420
QY	421	CTATCTCG	GAACATTA	CCAA	CGCCAGCGT	CTGTGTAC	CCAGCATTTGCTGG	480
Db	421	CTATCTCG	GAACATTA	CCAA	CGCCAGCGT	CTGTGTAC	CCAGCATTTGCTGG	480
QY	481	CTGGCCG	GAAGTGGTCA	AGTCCG	GAATTA	TGCTGATG	TCAGACGAGCA	540
Db	481	CTGGCCG	GAAGTGGTCA	AGTCCG	GAATTA	TGCTGATG	TCAGACGAGCA	540

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QY 541 AGGCGAAGCCTTGGCCGCGGCTGGAAGCTGACCTGCAATTAACGTATACCAAGG 600
Db 541 AGGCGAAGCCTTGGCCGCGGCTGGAAGCTGACCTGCAATTAACGTATACCAAGG 600
QY 601 AGATACGTCCAGTCCGATCCGATTTATTAATCTCTAAAACTGGCGTTGCCAATGGA 660
Db 601 AGATACGTCCAGTCCGATCCGATTTATTAATCTCTAAAACTGGCGTTGCCAATGGA 660
QY 661 TAAAGCGAAGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 720
Db 661 TAAAGCGAAGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 720
QY 721 CGGGGATCGGCAACCGGCTTCCGCAACTGGAACGGGTCTTAATTTTCCGCAATGAA 780
Db 721 CGGGGATCGGCAACCGGCTTCCGCAACTGGAACGGGTCTTAATTTTCCGCAATGAA 780
QY 781 CTGTGCTTAAACGTGAGAAACAGACGAAAGCTGTTCAATTAACGCAAGCATTAACATC 840
Db 781 CTGTGCTTAAACGTGAGAAACAGACGAAAGCTGTTCAATTAACGCAAGCATTAACATC 840
QY 841 GGAATCTAAGGTGAGCGCGCAATGCTCATTAACCGGTGCGTAAAGCTCGCATCAAT 900
Db 841 GGAATCTAAGGTGAGCGCGCAATGCTCATTAACCGGTGCGTAAAGCTCGCATCAAT 900
QY 901 GCTGACGAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGCGGAGGAGGAG 960
Db 901 GCTGACGAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGCGGAGGAGGAG 960
QY 961 GATCACCATTTACACCAAGTGAACACTTGTGATTAAGTGAACGCGCAATTTATTT 1020
Db 961 GATCACCATTTACACCAAGTGAACACTTGTGATTAAGTGAACGCGCAATTTATTT 1020
QY 1021 GCTACACGACGACGAGGTTGCCGAGCGCGGCAAGCGCGGCAAGTTGATCA 1080
Db 1021 GCTACACGACGACGAGGTTGCCGAGCGCGGCAAGCGCGGCAAGTTGATCA 1080
QY 1081 GACAGCGTTGACGCGGCTTCCAGCGCAAAACAGCGGCTGATGACATTAACCATCTC 1140
Db 1081 GACAGCGTTGACGCGGCTTCCAGCGCAAAACAGCGGCTGATGACATTAACCATCTC 1140
QY 1141 AGTGTCTTTATCGCGGCAACAGATTAATCTGCAATCTCGGCGCGCATGAGACT 1200
Db 1141 AGTGTCTTTATCGCGGCAACAGATTAATCTGCAATCTCGGCGCGCATGAGACT 1200
QY 1201 CAATGAGAGCTTCCCGGTCAAGCGGATTAACAGCGCGGCAAGTGTGAACTGTGTTGA 1260
Db 1201 CAATGAGAGCTTCCCGGTCAAGCGGATTAACAGCGCGGCAAGTGTGAACTGTGTTGA 1260
QY 1261 AGCTGAGCGGTGAGGATTAACAGCGGATTAACAGCGGATTAACAGCGGATTAACAG 1320
Db 1261 AGCTGAGCGGTGAGGATTAACAGCGGATTAACAGCGGATTAACAGCGGATTAACAG 1320
QY 1321 TTTACAGAGATGCTGATTAACAGCGGCTGCTATTAATAAGCGCGCGAGAGGTGA 1380
Db 1321 TTTACAGAGATGCTGATTAACAGCGGCTGCTATTAATAAGCGCGCGAGAGGTGA 1380
QY 1381 ACTGACCTGAGAGATGAGAGAGAGAAATGCGAGGCGATGTGTGTGGGAGGTTT 1440
Db 1381 ACTGACCTGAGAGATGAGAGAGAGAAATGCGAGGCGATGTGTGTGGGAGGTTT 1440
QY 1441 TACGCAATCTGATTAAGAGAGAGATTAACGCGGTGCAATTTGATGATTAATAAAG 1500
Db 1441 TACGCAATCTGATTAAGAGAGAGATTAACGCGGTGCAATTTGATGATTAATAAAG 1500
QY 1501 CATTCAGTTAAGTGAATGCTTGAAGCTGATGAACAAAGAAATGCTTAATGCTGA 1560
Db 1501 CATTCAGTTAAGTGAATGCTTGAAGCTGATGAACAAAGAAATGCTTAATGCTGA 1560
QY 1561 CGGGAAGAGCGGCTTCAAGCGGATCCGCGCACTTCACTTTCTCTTCTGAGTAAC 1620
Db 1561 CGGGAAGAGCGGCTTCAAGCGGATCCGCGCACTTCACTTTCTCTTCTGAGTAAC 1620

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QY 1621 TATAACCGTAATAGTTATAGCCGTAAGCTGTAAGCGGCTGCTGCTTAACTACACCAT 1680
Db 1621 TATAACCGTAATAGTTATAGCCGTAAGCTGTAAGCGGCTGCTGCTTAACTACACCAT 1680
QY 1681 TGAAGATAGCGCTTATATTAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 TGAAGATAGCGCTTATATTAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 CCTCTTGGCGGCTTCAAGCGCAAAACGCGAACCAGAGGCTGCTGCTGCTGCTGCTGCT 1800
Db 1741 CCTCTTGGCGGCTTCAAGCGCAAAACGCGAACCAGAGGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 CCAAGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1801 CCAAGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1861 AATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901
Db 1861 AATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901

RESULT 6
US-10-284-962-4
; Sequence 4, Application US/10284962
; Publication No. US20030206913A1
; GENERAL INFORMATION:
; APPLICANT: Webel, Douglas M.
; APPLICANT: Orr, Donald E.
; APPLICANT: Ruch, Frank E.
; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
; FILE REFERENCE: 834460-71725
; CURRENT APPLICATION NUMBER: US/10/284,962
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/335,303
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (188)..(1483)
; OTHER INFORMATION:
US-10-284-962-4

Query Match 75.8%; Score 1440.2; DB 16; Length 1486;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 TAAAGAGCAAGAACATGATGATGATTAATTAATGATGATGATGATGATGATGATGATG 60
Db 1 TAAAGAGCAAGAACATGATGATGATTAATTAATGATGATGATGATGATGATGATGATG 60
QY 61 CTCTCCACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 61 CTCTCCACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 TGAATGCGGCGCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 TGAATGCGGCGCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 CATATGATGAAAGCGATCTTAATCCCATTTTATCTCTTGTATTCGTTAAACCCGCA 240
Db 181 CATATGATGAAAGCGATCTTAATCCCATTTTATCTCTTGTATTCGTTAAACCCGCA 240
QY 241 ATCTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 241 ATCTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 TCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

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Db	595	AGATAGCTCCAGTCCCGATCCCGTATTATATCTCTTAATAAACTGGCGTTTCCCACTGGA	655
Qy	661	TAAACGGAAACGTGACTGACACGCCATCTCAGCAGGGCAGAGGGGTCAATTGCTGACTTTAC	722
Db	655	TAAACGGAAACGTGACTGACGCCATCTCAGCAGGGCAGAGGGGTCAATTGCTGACTTTAC	714
Qy	721	CGGGCATCGGCAAAACGGCGTTTCGCAATGTGAACGGGTCCTAATTTTTCGCAATCAA	786
Db	715	CGGGCATCGGCAAAACGGCGTTTCGCAATGTGAACGGGTCCTAATTTTTCGCAATCAA	774
Qy	781	CTTGTGCTTTAAACGTGAGAAACAGACGAACCTGTTTCAATTACGACGGCATTAACATC	846
Db	775	CTTGTGCTTTAAACGTGAGAAACAGACGAACCTGTTTCAATTACGACGGCATTAACATC	834
Qy	841	GGAACCTCAAGTGTAGCGCGGCAACATGTCTCATTTAACCGGTGGGTAAAGCTTCGATCAT	900
Db	835	GGAACCTCAAGTGTAGCGCGGCAACATGTCTCATTTAACCGGTGGGTAAAGCTTCGATCAT	899
Qy	901	GCTGACGGAGATATTTCTCTCTGACACAGACAAGGGAATGCCGAGCCGGGTGGGGAG	966
Db	895	GCTGACGGAGATATTTCTCTCTGACACACAGGAATGCGGAGCCGGGTGGGGAG	954
Qy	961	GATCACCGAATTTCACCAAGTGAACACCTGTGTAAGTTGTGATTAACGCGCAATTTATTT	1022
Db	955	GATCACCTGATTCACCAAGTGAACACCTGTGTAAGTTGTGATTAACGCGCAATTTATTT	1010
Qy	1021	GCTPACAAACGACGCGCAGAGGTTGCCCGACGCCGCAACCCGTATTATTAATTGATCAA	1086
Db	1015	ACTPACAAACGACGCGCAGAGGTTGCCCGAGTGGCGCACCCCGTATTATTAATTGATCAT	1074
Qy	1081	GATCAGGTTGACGCGCCCATCTCAACGCAAAAACAGGCGATGTGTTGATTAACCACTTC	1147
Db	1075	GATCAGGTTGACGCGCCCATCTCAACGCAAAAACAGGCGATGTGTTGATTAACCACTTC	1135
Qy	1141	AGTGTGTTTATGCGCGGACACGATATCTAATCTGGCAATCTCGCGCGCATGTGAAGCT	1207
Db	1135	AGTGTGTTTATGCGCGGACACGATATCTAATCTGGCAATCTCGCGCGCATGTGAAGCT	1193
Qy	1201	CAACTGGACGCTCCCGGTCACGCGGATGAACAGCGGCAAGGTGGTAACTGTGTTTGA	1268
Db	1195	CAACTGGACGCTCCCGGTCACAGTCGGATTAACAGCGGCAAGGTGGTAACTGTGTTTGA	1256
Qy	1261	ACGCTGGCGCTCGGCTTAAGCATTAACAGCCAGTGAATTCAAGTTTGGCTGTTTCAAC	1328
Db	1255	ACGCTGGCGCTCGGCTTAAGCATTAACAGCCAGTGAATTCAAGTTTGGCTGTTTCAAC	1316
Qy	1321	TTTACACGCAATGCGGATTAACACGCGCGTCATTTAATAGCGCGCCCGGAGAGGTGAA	1383
Db	1315	TTTACACGCAATGCGGATTAACACGCGCGTCATTTAATAGCGCGCCCGGAGAGGTGAA	1303
Qy	1381	ACTGACCTTGGCAGATGTGAAGAGCGAATGCGAGGGCATGTTCGTTGCAAGTTT	1444
Db	1375	ACTGACCTTGGCAGATGTGAAGAGCGAATGCGAGGGCATGTTCGTTGCAAGTTT	1432
Qy	1441	TAGGCAAAATGTGAATGAAGCACGCACTACCGCGTGCAGTTTGTATG	1488
Db	1435	TAGGCAAAATGTGAATGAAGCGCACATCCGCGGTGACGATTTGTATG	1482

RESULT 8
 US-10-284-962-1
 ; Sequence 1, Application US/10284962
 ; Publication No. US20030206913A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Webel, Douglas M.
 ; APPLICANT: Orr, Donald E.
 ; APPLICANT: Ruch, Frank E.
 ; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
 ; FILE REFERENCE: 834460-7125
 ; CURRENT APPLICATION NUMBER: US/10/284,962
 ; CURRENT FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: US 60/335,303

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1 PRIOR FILING DATE: 2001-10-31
2 NUMBER OF SEQ ID NOS: 14
3 SOFTWARE: PatentIn version 3
4 SEQ ID NO 1
5     LENGTH: 1489
6     TYPE: DNA
7     ORGANISM: Escherichia coli
8     FEATURE:
9     NAME/KEY: primer_bind
10    LOCATION: (1)..(32)
11    OTHER INFORMATION:
12    FEATURE:
13    NAME/KEY: primer_bind
14    LOCATION: (1468)..(1489)
15    OTHER INFORMATION:
16    FEATURE:
17    NAME/KEY: CDS
18    LOCATION: (16)..(108)
19    OTHER INFORMATION:
20    FEATURE:
21    NAME/KEY: CDS
22    LOCATION: (182)..(1480)
23    OTHER INFORMATION:
24    JS-10-284-962-1

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Query Match	73.5%	Score 1397.4	DB 16	Length 1489
Best Local Similarity	97.1%	Pred. No. 0		
Matches 145;	Conservative 0	Mismatches 37	Indels 6	Gaps 2

Qy	1	TAAAGAGCAAGAAACATGGATATTTACCTTGGATTCGCGCATTTTGTGATGTGTGCG	60
Db	1	TAAAGAGCAAGAAACATGGATATTTCCCTTTGTGTTCTGTGCGCATTTTGTGATGTGTGCG	60
Qy	61	CTCTCCACCTTGTGTGTGGATATGCTGGAACCGCGCTGAAAAAGTTAACGAACGTAGCC	120
Db	61	CTCTCCACCTTGTGTGTGGATATGCGTGAACCGCGCATGAAAAAGTTAACGAACGTAGCC	120
Qy	121	TGATGCGGCGCATTTAGCATATGCAATCAGGCAATCAATAATGTCAGATATGAAAAAGCGAAA	180
Db	121	TGATCCGCGCGCATTTAGCGTGC-----ATCAGGCAATAATATGGAATAT-CAAAAGCGAAA	178
Qy	181	CATATGATGAAGAGCATTTATATCCCATTTTATCTCTTCTGATTCGGTTAAACCCCGCA	240
Db	175	CATATGATGAAGAGCGATTTATATCCCATTTTATCTCTTGTGATTCGGTTAAACCCCGCA	234
Qy	241	ATCTGCATTGCGCTCAGATGAGACCCGAGCTGAGCTGGAAGATGTGATTTGTCAGTGC	300
Db	235	ATCTGCATTGCGTCAAGATGAGCCCGAGCTGAGCTGGAAGTGTGATTTGTCAGCTGC	294
Qy	301	TCTATGTTGTGCTGTCTCCAAACCAAGGCCAAGCACTGATGAGAGATGCAACCCAGAGCG	360
Db	295	TCTATGTTGTGCTGTGCCCCCAACCAAGGCCAAGCACTGATGAGAGATGCAACCCAGAGCG	358
Qy	361	ATGAGCAACCTGAGCGGTAAACTGAGGATTTGCTGACACCGAGAGTGTGACTAATGCG	420
Db	355	ATGAGCAACCTGAGCGGTAAACTGAGGATTTGCTGACACAGCGGTGTGAGCTAATGCG	414
Qy	421	CTATCTCGAGCAATTATCAAGGCAAGCGTCTGGTAGCGACGAGATTGCTGCGGAAAAAAGG	480
Db	415	CTATCTCGAGCAATTATCAAGGCAAGCGTCTGGTAGCGACGAGATTGCTGCGGAAAAAAGG	478
Qy	481	CTGCCCCGACAGTGTGTCAGATCGCATTAATGCTGATGTGACAGAGCGTACCCGTAATAC	540
Db	475	CTGCCCCGACGCTGTGTCAGATCGCATTAATGCTGATGTGACAGAGCGTACCCGTAATAC	534
Qy	541	AGGCGAAGCCTTGTGCGCGCGGCTGAGCACTGATCTCAATTAACCGTACATACCCAGGC	600
Db	535	AGGCGAAGCCTTGTGCGCGCGGCTGAGCACTGATCTGCAATTAACCGTACATACCCAGGC	594
Qy	601	AGATAGCTCCAGTCCGATCCGATTTATTAATCTCTTAATAACTGCGCTTGTCCCAACTGGA	660
Db	595	AGATAGCTCCAGTCCGATCCGATTTATTAATCTCTTAATAACTGCGCTTGTCCCAACTGGA	654

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QY 661 TAACGCGAAGCTGACGCGGATCTTCAGCAGGCGAGGAGGCAATTGCTGACCTTAC 720
Db 655 TAACGCGAAGCTGACGCGGATCTTCAGCAGGCGAGGAGGCAATTGCTGACCTTAC 724
QY 721 CGGGCATCGGCAACGGGCTTCCGGAAGTGGAACTGGTAATTTCCGCAATCAA 780
Db 715 CGGGCATCGGCAACGGGCTTCCGGAAGTGGAACTGGTAATTTCCGCAATCAA 774
QY 781 CTGTGCTTAAAGCTGAGAAACAGAACGAAAGCTGTTCATTAAACGAGCATTAACATC 840
Db 775 CTGTGCTTAAAGCTGAGAAACAGAACGAAAGCTGTTCATTAAACGAGCATTAACATC 834
QY 841 GGAATTCAGGTGAGCGCGCAATGTCTCATTAACCGGTGCGGTAAAGCTCGATCAAT 900
Db 835 GGAATTCAGGTGAGCGCGCAATGTCTCATTAACCGGTGCGGTAAAGCTCGATCAAT 894
QY 901 GCTGACGAGATATTTCTCTGCAACAGCAACAGGAAATGCGGAGCGGCGGTGGAG 960
Db 895 GCTGACGAGATATTTCTCTGCAACAGCAACAGGAAATGCGGAGCGGCGGTGGAG 954
QY 961 GATCAGCATTCACACCGAGTGAACCTTGTCTAATGTTGATTAACGCGCATTTATTT 1020
Db 955 GATCAGCATTCACACCGAGTGAACCTTGTCTAATGTTGATTAACGCGCATTTATTT 1014
QY 1021 GCTACAAACGACGCGAGAGTTCGCGAGCGCGCCACCGCTTATTAGATTGATCAA 1080
Db 1015 ACTACAAACGACGCGAGAGTTCGCGAGCGCGCCACCGCTTATTAGATTGATCAT 1074
QY 1081 GACAGCGTTGACGCGCATTCACCGCAAAAACGCGGTATGCTGATTAACCACTTC 1140
Db 1075 GACAGCGTTGACGCGCATTCACCGCAAAAACGCGGTATGCTGATTAACCACTTC 1134
QY 1141 AGTGTCTTTATTCGCGGACAGCATTAATCTGGCAAAATCGCGCGCGCATGAGCT 1200
Db 1135 AGTGTCTTTATTCGCGGACAGCATTAATCTGGCAAAATCTGGCGCGCATGAGCT 1194
QY 1201 CAATGACGCTTCCCGGTACGCGCGATTAACACGCGCGAGTGTGATGTTGA 1260
Db 1195 CAATGACGCTTCCCGGTACGCGCGATTAACACGCGCGAGTGTGATGTTGA 1254
QY 1261 ACGTGGCGTGGCTTAAGCGATTAACGACGATTAAGTTGCTGCTGCTCCAGAC 1320
Db 1255 ACGTGGCGTGGCTTAAGCGATTAACGACGATTAAGTTGCTGCTGCTCCAGAC 1314
QY 1321 TTTCAGAGATGCTGTATTAACGCGCGCTGTATTAATAACGCGCGAGAGGTGAA 1380
Db 1315 TTTCAGAGATGCTGTATTAACGCGCGCTGTATTAATAACGCGCGAGAGGTGAA 1374
QY 1381 ACTGACCGTGGAGATGTAAGAGCGGAATGCGAGGCGCATGTCTGCTGCAAGTTT 1440
Db 1375 ACTGACCGTGGAGATGTAAGAGCGGAATGCGAGGCGCATGTCTGCTGCAAGTTT 1434
QY 1441 TACGCAATCGTGAATGAAGACGCAATCGCGCTGCTGATTTGTAATG 1488
Db 1435 TACGCAATCGTGAATGAAGAGCGCGCATCGCGCTGCTGATTTGTAATG 1482

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RESULT 9

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US-10-282-122A-7167
; Sequence 7167, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.

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; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PENDING FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 7167
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-282-122A-7167

Query Match 68.3%; Score 1298; DB 13; Length 1299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1298; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 188 ATGAAGCATCTTAATCCCATTTTATCTCTGATTCGTTAACCCCGCATCTGCA 247
Db 1 ATGAAGCATCTTAATCCCATTTTATCTCTGATTCGTTAACCCCGCATCTGCA 60
QY 248 TTGCTCAAGTGAAGCGGAGCTGAAGCTGGAAGTGTGTATTTGTCTATGTGT 307
Db 61 TTGCTCAAGTGAAGCGGAGCTGAAGCTGGAAGTGTGTATTTGTCTATGTGT 120
QY 308 GTGCGTCTCAACCAAGGCGCAACGCAATGATGACAGATGACACCCGACATGGCA 367
Db 121 GTGCGTCTCAACCAAGGCGCAACGCAATGATGACAGATGACACCCGACATGGCA 180
QY 368 ACTGCGCGGTAAACTGGGTGCTGACACCGGAGGTGTGAGCTAATGCTATCTC 427
Db 181 ACTGCGCGGTAAACTGGGTGCTGACACCGGAGGTGTGAGCTAATGCTATCTC 240
QY 428 GGCATTAACCAACGCGAGGCTGAGTGAAGCGGAGATGCTGCGCAAAAAGGGCTGCCG 487
Db 241 GGCATTAACCAACGCGAGGCTGAGTGAAGCGGAGATGCTGCGCAAAAAGGGCTGCCG 300
QY 488 CAGTGTGTCAGGTGCGATTAATGCTGATGTGACAGAGGTAACCGTAAACAGGCGAA 547
Db 301 CAGTGTGTCAGGTGCGATTAATGCTGATGTGACAGAGGTAACCGTAAACAGGCGAA 360
QY 548 GCGTTCGCGCGCGGCTGCGACCTGACTGTGAATTAACCTGATCAATACCGAGCATAGG 607
Db 361 GCGTTCGCGCGCGGCTGCGACCTGACTGTGAATTAACCTGATCAATACCGAGCATAGG 420
QY 608 TCCAGTCCGATCCGTTATTAATCTCTAATAAATGCGGCTTGCACATGATTAACGCG 667
Db 421 TCCAGTCCGATCCGTTATTAATCTCTAATAAATGCGGCTTGCACATGATTAACGCG 480
QY 668 AACGTACAGAGCGGATCTCTGACAGAGGCGAGAGGCTCAATGCTGATTAACGCGGAT 727
Db 481 AACGTACAGAGCGGATCTCTGACAGAGGCGAGAGGCTCAATGCTGATTAACGCGGAT 540

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QY 728 CGGCAAAAGGGGTTTCGGAACTGGAACGGGTCCTTAATTTTCCGCAATCAACTTGTGC 787
DB 541 CGGCAAAAGGGGTTTCGGAACTGGAACGGGTCCTTAATTTTCCGCAATCAACTTGTGC 600
QY 788 CTTAAACGTGAGAAACGAGACGAAAGCTGTTCATTAAAGCAGAGCTTACCTCGAACTC 847
DB 601 CTTAAACGTGAGAAACGAGACGAAAGCTGTTCATTAAAGCAGAGCTTACCTCGAACTC 660
QY 848 AAGGTGAGCGCCGCAATGTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 907
DB 661 AAGGTGAGCGCCGCAATGTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 720
QY 908 GAGATATTTCTCTGCAACGACGAGGGAATGCGGAGCGGGGTGGGGAAGGATCACG 967
DB 721 GAGATATTTCTCTGCAACGACGAGGGAATGCGGAGCGGGGTGGGGAAGGATCACG 780
QY 968 GATTCAACCAAGTGAACACCTTGTGAAGTTGATTAACGCGCAATTTTATTGTCTACAA 1027
DB 781 GATTCAACCAAGTGAACACCTTGTGAAGTTGATTAACGCGCAATTTTATTGTCTACAA 840
QY 1028 CGCAGCGCGAGGTTGCCCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1087
DB 841 CGCAGCGCGAGGTTGCCCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 1088 TTGACGCGCCCATCAACCGCAAAACAGGCGTATGATGATTAACCACTTCAAGTCTG 1147
DB 901 TTGACGCGCCCATCAACCGCAAAACAGGCGTATGATGATTAACCACTTCAAGTCTG 960
QY 1148 TTTATTCGCGGACAGATTAATCTGGAATCTTCGCGCGCGCGCGCGCGCGCGCGCG 1207
DB 961 TTTATTCGCGGACAGATTAATCTGGAATCTTCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1208 AGCTTCGCGGTCAAGCGGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
DB 1021 AGCTTCGCGGTCAAGCGGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
QY 1268 CGTCCGCTTAAGGATTAACGCGCGGATTAACGCGGTTTCGCTGCTTCAAGCTTAC 1327
DB 1081 CGTCCGCTTAAGGATTAACGCGCGGATTAACGCGGTTTCGCTGCTTCAAGCTTAC 1140
QY 1328 CAGATGCGGATTAACGCGGCTGTTCATTAAATAGCGCGCGCGGAGAGTGAATGAC 1387
DB 1141 CAGATGCGGATTAACGCGGCTGTTCATTAAATAGCGCGCGCGGAGAGTGAATGAC 1200
QY 1388 CTGGCAGATGTGAAGAGGAAATGCGCAGGCGCATGTGTTGTTGCGAGTTTACGCA 1447
DB 1201 CTGGCAGATGTGAAGAGGAAATGCGCAGGCGCATGTGTTGTTGCGAGTTTACGCA 1260
QY 1448 ATCGTGAATGAAGCAGCATACCGCGCTGCACTTTGTA 1486
DB 1261 ATCGTGAATGAAGCAGCATACCGCGCTGCACTTTGTA 1299

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RESULT 10
US-09-777-566A-1
; Sequence 1, Application US/0977566A
; Patent No. US20010055788A1
;
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: KREIZ, Kelch
; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
; FILE REFERENCE: DIVER1370-6
; CURRENT APPLICATION NUMBER: US/09/777,566A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: US 09/259,214
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/910,798

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; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1320)
; NAME/KEY: misc_feature
; LOCATION: (1)..(1323)
; OTHER INFORMATION: n is any nucleotide
US-09-777-566A-1

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Query Match      67.7%; Score 1287.8; DB 9; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 188 ATGAAAGCGATCTTAATCCATTTTATCTTCTGATTCGTTAACCCCGCAATCTGCA 247
DB 1 ATGAAAGCGATCTTAATCCATTTTATCTTCTGATTCGTTAACCCCGCAATCTGCA 60
QY 248 TTGCTCTCAGATGAGCCGCGAGCTGAAGCTGGAAGTGTGTGATTTGTCACTGTGAT 307
DB 61 TTGCTCTCAGATGAGCCGCGAGCTGAAGTGTGTGATTTGTCACTGTGAT 120
QY 308 GTGCTGCTCAACCAAGGCGCAAGCTGATGACAGATGTCACCCGACGATGCGCA 367
DB 121 GTGCTGCTCAACCAAGGCGCAAGCTGATGACAGATGTCACCCGACGATGCGCA 180
QY 368 ACCTGGCGGTTAAACTGGGTTGGCTGACACCGCGGTTGGTGAAGTTATCGCTATCTC 427
DB 181 ACCTGGCGGTTAAACTGGGTTGGCTGACACCGCGGTTGGTGAAGTTATCGCTATCTC 240
QY 428 GGAATTACCAAGCGCAGGCTGTGATGACGAGATGCGGCGAAATGCGGAAAGGGCTGCG 487
DB 241 GGAATTACCAAGCGCAGGCTGTGATGACGAGATGCGGCGAAATGCGGAAAGGGCTGCG 300
QY 488 CAGTCTGTGAGGTGCGGATTAATGCTGATGTCAGAGCGTACCCGTAACAGCGCAA 547
DB 301 CAGTCTGTGAGGTGCGGATTAATGCTGATGTCAGAGCGTACCCGTAACAGCGCAA 360
QY 548 GCTTGGCGCGCGGCTGCGACCTGACTGTGCAATTAACGTTACATCCAGGAGATAG 607
DB 361 GCTTGGCGCGCGGCTGCGACCTGACTGTGCAATTAACGTTACATCCAGGAGATAG 420
QY 608 TCCAGTCCCGATCCGTTATTTAATCCTTAATAAATGCGGTTTCCCACTGATTAACGCG 667
DB 421 TCCAGTCCCGATCCGTTATTTAATCCTTAATAAATGCGGTTTCCCACTGATTAACGCG 480
QY 668 AAGCTGACTAGCGGATCTTCAGAGAGGCGAGAGGCTCAATTGCTGACTTTACGGGCA 727
DB 481 AAGCTGACTAGCGGATCTTCAGAGAGGCGAGAGGCTCAATTGCTGACTTTACGGGCA 540
QY 728 CGGCAACGCGCGTTTTCGCAACTGGAACGCGGCTCTTAATTTTCGCAATCAACTTGTGC 787
DB 541 CGGCAACGCGCGTTTTCGCAACTGGAACGCGGCTCTTAATTTTCGCAATCAACTTGTGC 600
QY 788 CTTAAACGTGAGAAACGAGACGAAAGCTGTTCATTAAAGCAGAGCTTACCTCGAACTC 847
DB 601 CTTAAACGTGAGAAACGAGACGAAAGCTGTTCATTAAAGCAGAGCTTACCTCGAACTC 660
QY 848 AAGGTGAGCGCCGCAATGTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 907
DB 661 AAGGTGAGCGCCGCAATGTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 720
QY 908 GAGATATTTCTCTGCAACGACGAGGGAATGCGGAGCGGGGTGGGGAAGGATCACG 967
DB 721 GAGATATTTCTCTGCAACGACGAGGGAATGCGGAGCGGGGTGGGGAAGGATCACG 780
QY 968 GATTCAACCAAGTGAACACCTTGTGAAGTTGATTAACGCGCAATTTTATTGTCTACAA 1027

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DB 781 GATTACACCAAGTGAACACCTGTAAGTTGATACGCGCAATTTATTTGTAACA 840
QY 1028 CGCAGCGCAAGAGTTGGCCCGGACCGCCGCAACCCCTTATTAATTTGATCAAGAGCG 1087
DB 841 CGCAGCGCAAGAGTTGGCCCGGACCGCCGCAACCCCTTATTTGATCAAGAGCG 900
QY 1088 TTGACGCCCGCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCACTGCTG 1147
DB 901 TTGACGCCCGCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCACTG 960
QY 1148 TTATTCGCGGACACGATTAATCTGCAATTTCCGCGCGGACGACGAGCTCACTG 1207
DB 961 TTATTCGCGGACACGATTAATCTGCAATTTCCGCGCGGACGACGAGCTCACTG 1020
QY 1208 ACGGTTCCCGGTCAGCGCGGATTAACAGCGCGGATGATGTAATCTGATTTGAACGCTG 1267
DB 1021 ACGGTTCCCGGTCAGCGCGGATTAACAGCGCGGATGATGTAATCTGATTTGAACGCTG 1080
QY 1268 CGTCGGCTAAGCGATTAACAGCGCGGATGATGTAATCTGATTTGAACGCTG 1327
DB 1081 CGTCGGCTAAGCGATTAACAGCGCGGATGATGTAATCTGATTTGAACGCTG 1140
QY 1328 CAGATGCGGTAAAGCGCGGTGATTAATACGCGCGGATGATGTAATCTGATTTGAACGCTG 1387
DB 1141 CAGATGCGGTAAAGCGCGGTGATTAATACGCGCGGATGATGTAATCTGATTTGAACGCTG 1200
QY 1388 CTGGCAGGATGTAAGAGCGGAATGCGAGGCGATGTTGTTGGAGGTTTGAACG 1447
DB 1201 CTGGCAGGATGTAAGAGCGGAATGCGAGGCGATGTTGTTGGAGGTTTGAACG 1260
QY 1448 ATCGGATGAAGACGCGATCCGCGCGTGAATTTGAT 1487
DB 1261 ATCGGATGAAGACGCGATCCGCGCGTGAATTTGAT 1300

RESULT 11
US-09-866-379-1
Sequence 1, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KREIZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARRON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHAGES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.1
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1323)
OTHER INFORMATION: n is any nucleotide
NAME/KEY: CDS
LOCATION: (1)..(1323)

OTHER INFORMATION:

US-09-866-379-1

Query Match 67.7%; Score 1287.8; DB 9; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0;
Matches 1293; Conservative 0

QY 188 ATGAAGGAGATCTTAATCCATTTTATCTCTTGATTCGCTTAACCCCGCAATCTGCA 247
DB 1 ATGAAGGAGATCTTAATCCATTTTATCTCTTGATTCGCTTAACCCCGCAATCTGCA 60
QY 248 TTGCTCAGAGTGAAGCCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 307
DB 61 TTGCTCAGAGTGAAGCCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
QY 308 GTGCGTGTCCCAACCAAGGCGCAAGCACTGATGAGATGCAACCCAGACGATGCGCA 367
DB 121 GTGCGTGTCCCAACCAAGGCGCAAGCACTGATGAGATGCAACCCAGACGATGCGCA 180
QY 368 ACGTGGCCGCTAAACTGGGTGCTGACACCGGNGGTGAGTGAATGCGCTATCTC 427
DB 181 ACGTGGCCGCTAAACTGGGTGCTGACACCGGNGGTGAGTGAATGCGCTATCTC 240
QY 428 GGAATTAACCAAGCGCAGGCTGCTGAGCGAGATTTGTCGCAAAAAGGCGTGGCCG 487
DB 241 GGAATTAACCAAGCGCAGGCTGCTGAGCGAGATTTGTCGCAAAAAGGCGTGGCCG 300
QY 488 CAGTGTGTGAGTGGCATTTTGTGATGTCGACGAGCGTAAACCCGTTAAACAGGCGAA 547
DB 301 CAGTGTGTGAGTGGCATTTTGTGATGTCGACGAGCGTAAACCCGTTAAACAGGCGAA 360
QY 548 GCCTTGCGCGCGGCGTGGCACTGATGTCGATTAACCGATACCAAGCAGATACG 607
DB 361 GCCTTGCGCGCGGCGTGGCACTGATGTCGATTAACCGATACCAAGCAGATACG 420
QY 608 TCCAGTCCCGATCCGTTATTTATCTCTTAATAAATCGCGCTTGGCACTGATACCGG 667
DB 421 TCCAGTCCCGATCCGTTATTTATCTCTTAATAAATCGCGCTTGGCACTGATACCGG 480
QY 668 AACGTACTGACGCGATCTCTGACAGGCGAGGAGGATGCTGATTAACCGGCGAT 727
DB 481 AACGTACTGACGCGATCTCTGACAGGCGAGGAGGATGCTGATTAACCGGCGAT 540
QY 728 CGGCAAAAGCGGCTTGGCACTGAAAGCGGCTGTTAATTTTCGCAATCAACTTGGC 787
DB 541 CGGCAAAAGCGGCTTGGCACTGAAAGCGGCTGTTAATTTTCGCAATCAACTTGGC 600
QY 788 CTTAAACGTGAAGAAACAGGACGAAGCTGTGATTAACGACGATTAACGATCGAATC 847
DB 601 CTTAAACGTGAAGAAACAGGACGAAGCTGTGATTAACGACGATTAACGATCGAATC 660
QY 848 AAGGTAGGCGCGCAATGCTCATTTAACCGGTGCGTAAAGCTCGCATCAATGCTGAG 907
DB 661 AAGGTAGGCGCGCAATGCTCATTTAACCGGTGCGTAAAGCTCGCATCAATGCTGAG 720
QY 908 GAGATATTTCTCTGGAAGAAGAGGAGATGCGGAGCCGCGGATGCGGAGAGATCAC 967
DB 721 GAGATATTTCTCTGGAAGAAGAGGAGATGCGGAGCCGCGGATGCGGAGAGATCAC 780
QY 968 GATTACACCAAGTGAACCTTGTAGTTGATTAACGCGCAATTTATTTGCTACAA 1027
DB 781 GATTACACCAAGTGAACCTTGTAGTTGATTAACGCGCAATTTATTTGCTACAA 840
QY 1028 CGCAGCGCAAGGTGCGCGGACCGCGCAACCCGTTATTTGATTTGAACAGAGG 1087
DB 841 CGCAGCGCAAGGTGCGCGGACCGCGCAACCCGTTATTTGATTTGAACAGAGG 900
QY 1088 TTGACGCCCGCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCACTGCTG 1147
DB 901 TTGACGCCCGCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCACTGCTG 960
QY 1148 TTATTCGCGGACACGATTAATCTGCAATTTCCGCGCGGACGACGAGCTCACTG 1207

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Db      961 TTATATCCGACACAGATACCTAATCTGCGAATCTCGCGCGGACACTGAGCTCAACTCG 1020
Qy      1208 ACGCTTCCCGGTACCGCGGATTAACACGCCGCCAGGTGGTGAATCTGTGTTGAAGCTGG 1267
Db      1021 ACGCTTCCCGGTACCGCGGATTAACACGCCGCCAGGTGGTGAATCTGTGTTGAAGCTGG 1080
Qy      1268 CGTGGCGTAAAGGATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1327
Db      1081 CGTGGCGTAAAGGATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1140
Qy      1328 CAGATGCGGTATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1387
Db      1141 CAGATGCGGTATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1200
Qy      1388 CTGGGAGAGTGTGAAGAGCGGAATGCGAGGCGAGTGTGTTGGCAGGTTTACGCA 1447
Db      1201 CTGGGAGAGTGTGAAGAGCGGAATGCGAGGCGAGTGTGTTGGCAGGTTTACGCA 1260
Qy      1448 ATCGTGAATGAAGACGACATACCGCGGTGCACTTTGTAAT 1487
Db      1261 ATCGTGAATGAAGACGACATACCGCGGTGCACTTTGTAAT 1300

RESULT 12
US-10-034-985-1
; Sequence 1, Application US/10034985
; Publication No. US2003004981S1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/034,985
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-034-985-1

Query Match      67.7%; Score 1287.8; DB 15; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db      181 ACCTGCGCGTAAACTGAGTTGGCTGACACGCGGNGTGTGAGCTAATCCCTATCTC 240
Qy      428 GGAATTATCCAAAGCCAGAGCTGTGTAGCGGACGGAATGCTGTGCGGAAAAAGGGCTGCCG 487
Db      241 GGAATTATCCAAAGCCAGAGCTGTGTAGCGGAGGATGTCTGCGGAAAAAGGGCTGCCG 300
Qy      488 CAGTGTGTGAGTTCGATTAATTTGCTGATGTGACGAGCGTAAACCGGTAAACAGGCGAA 547
Db      301 CAGTGTGTGAGTTCGATTAATTTGCTGATGTGACGAGCGTAAACCGGTAAACAGGCGAA 360
Qy      548 GCCTTGGCGCGCGGGCTGGGACCTGACTGTGCAATACCGTACATACCAGGACGATAG 607
Db      361 GCCTTGGCGCGCGGGCTGGGACCTGACTGTGCAATACCGTACATACCAGGACGATAG 420
Qy      608 TCCAGTCCCGATCGTTATTTAATCTCTTAAAACTGGGTTTCCCACTGATTAACGCG 667
Db      421 TCCAGTCCCGATCGTTATTTAATCTCTTAAAACTGGGTTTCCCACTGATTAACGCG 480
Qy      668 AACGTGACTGACGCGATCTTCAGACAGGCGAGAGGCTCAATTGCTGACTTTACCGGCA 727
Db      481 AACGTGACTGACGCGATCTTCAGACAGGCGAGAGGCTCAATTGCTGACTTTACCGGCA 540
Qy      728 CGGCAACCGCGCTTTCGCGAATCTGAAACGGGCTTAATTTTCGCAATCAACTGTGCG 787
Db      541 CGGCAACCGCGCTTTCGCGAATCTGAAACGGGCTTAATTTTCGCAATCAACTGTGCG 600
Qy      788 CTTAAACGTGAGAAACAGACGAAAGCTGTTCATTAACGAGGCAATTAACATCGAACTC 847
Db      601 CTTAAACGTGAGAAACAGACGAAAGCTGTTCATTAACGAGGCAATTAACATCGAACTC 660
Qy      848 AAGGTGAGCGCGGACATGTCTCATTTAACGGGTGCGGTAACTTCGATCAATGCTGACG 907
Db      661 AAGGTGAGCGCGGACATGTCTCATTTAACGGGTGCGGTAACTTCGATCAATGCTGACG 720
Qy      908 GAGATATTTCTCCGCAACAGACACAGGGAATCCGAGCGGAGTGGGAGAGATCAC 967
Db      721 GAGATATTTCTCCGCAACAGACACAGGGAATCCGAGCGGAGTGGGAGAGATCAC 780
Qy      968 GATTCAACCAAGTGAACACCTTGTCTTAAGTTTGCATTAACCGCGAATTTATTTGCTACAA 1027
Db      781 GATTCAACCAAGTGAACACCTTGTCTTAAGTTTGCATTAACCGCGAATTTATTTGCTACAA 840
Qy      1028 CGCAGCGCAGAGTGTGCGCGGACGCGGACCGCGCTTATTAATTTGATCAACAGACG 1087
Db      841 CGCAGCGCAGAGTGTGCGCGGACGCGGACCGCGCTTATTAATTTGATCAACAGACG 900
Qy      1088 TTGAACGCGCCATCCACCGCAAAACAGGCGTATGTGTGACATTAACCACTTACAGTCTG 1147
Db      901 TTGAACGCGCCATCCACCGCAAAACAGGCGTATGTGTGACATTAACCACTTACAGTCTG 960
Qy      1148 TTATATCCGCGGACAGATACCTAATCTGCGAATCTCGCGCGGCGACTGAGACTCACTGG 1207
Db      961 TTATATCCGCGGACAGATACCTAATCTGCGAATCTCGCGCGGCGACTGAGACTCACTGG 1020
Qy      1208 ACGCTTCCCGGTACCGCGGATTAACACGCCGCCAGGTGGTGAATCTGTGTTGAAGCTGG 1267
Db      1021 ACGCTTCCCGGTACCGCGGATTAACACGCCGCCAGGTGGTGAATCTGTGTTGAAGCTGG 1080
Qy      1268 CGTGGCGTAAAGGATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1327
Db      1081 CGTGGCGTAAAGGATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1140
Qy      1328 CAGATGCGGTATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1387
Db      1141 CAGATGCGGTATTAACAGCAGCTGATTCAGTTCAGTTCGCTGCTCTTCCAGACTTAAAG 1200
Qy      1388 CTGGGAGAGTGTGAAGAGCGGAATGCGAGGCGAGTGTGTTGGCAGGTTTACGCA 1447
Db      1201 CTGGGAGAGTGTGAAGAGCGGAATGCGAGGCGAGTGTGTTGGCAGGTTTACGCA 1260
Qy      1448 ATCGTGAATGAAGACGACATACCGCGGTGCACTTTGTAAT 1487
Db      1261 ATCGTGAATGAAGACGACATACCGCGGTGCACTTTGTAAT 1300

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RESULT 13
US-10-430-356-1
; Sequence 1, Application US/10430356
; Publication No. US20030232041A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/430,356
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1320)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-430-356-1

Query Match 67.7%; Score 1287.8; DB 16; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 188 ATGAAGGATCTTAATCCATTTTATCTTCTGATTCGGTTAACCCGCAATGCA 247
DB 1 ATGAAGGATCTTAATCCATTTTATCTTCTGATTCGGTTAACCCGCAATGCA 60
QY 248 TTGCTCAGAGTGAAGCCGAGCTGAAGCTGGAAGTGTGATTTGCACTGATGT 307
DB 61 TTGCTCAGAGTGAAGCCGAGCTGAAGCTGGAAGTGTGATTTGCACTGATGT 120
QY 308 GTGCGTGTCCAAACCAAGGCGCAAGCACTGATGAGGATGTCAACCCAGACGATGCGCA 367
DB 121 GTGCGTGTCCAAACCAAGGCGCAAGCACTGATGAGGATGTCAACCCAGACGATGCGCA 180
QY 368 ACTGAGCGGTAACCTGGGTGCTGACACCGCGAGGTGATGATTCGCTATCTC 427
DB 181 ACTGAGCGGTAACCTGGGTGCTGACACCGCGAGGTGATGATTCGCTATCTC 240
QY 428 GGAACCTTACCAAGCGCAGCGTCTGGTAGCGGACGGAATTGCTGGGAAAGGGCTGCCG 487
DB 241 GGAACCTTACCAAGCGCAGCGTCTGGTAGCGGACGGAATTGCTGGGAAAGGGCTGCCG 300
QY 488 CAGTCTGAGTGAAGTGCAGATTATGCTGATGTGACGAGCGTACCCGTAACAGCGGAA 547
DB 301 CAGTCTGAGTGAAGTGCAGATTATGCTGATGTGACGAGCGTACCCGTAACAGCGGAA 360
QY 548 GCGTTCGCGCGCGGCTGCGACCTGACCTGATGCAATTAACCGCAATACCCAGCGATACG 607
DB 361 GCGTTCGCGCGCGGCTGCGACCTGACCTGATGCAATTAACCGCAATACCCAGCGATACG 420
QY 608 TCCAGTCCCGATCCGTTATTTATCTCTTAAACTGGCGTTTGCAACTGGAATACGCG 667
DB 421 TCCAGTCCCGATCCGTTATTTATCTCTTAAACTGGCGTTTGCAACTGGAATACGCG 480

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QY 668 AACGTCCTGAAGGATCTCAGAGGAGGAGGTCATATGCTGACTTAAACCGGCGAT 727
DB 481 AACGTCCTGAAGGATCTCAGAGGAGGAGGTCATATGCTGACTTAAACCGGCGAT 540
QY 728 CGGCAAAACGGCGTTTCGGGAATCGGAACGGGTGCTTAATTTTCGGATCAAACTGTGC 787
DB 541 CGGCAAAACGGCGTTTCGGGAATCGGAACGGGTGCTTAATTTTCGGATCAAACTGTGC 600
QY 788 CTTAAACGTGAAGAAACAGGAGGAAGCTGCTTAACGAGGAGTAAACATCGGAATC 847
DB 601 CTTAAACGTGAAGAAACAGGAGGAAGCTGCTTAACGAGGAGTAAACATCGGAATC 660
QY 848 AAGTGAGCGCGCAATATGCTCATTTAACCGGTGCTTAACCGTCAATGCTGACG 907
DB 661 AAGTGAGCGCGCAATATGCTCATTTAACCGGTGCTTAACCGTCAATGCTGACG 720
QY 908 GAGTATTTTCTCTGCAACAGCAACGAGGAATGCCGAGCCGGGTGGGAAAGATCAC 967
DB 721 GAGTATTTTCTCTGCAACAGCAACGAGGAATGCCGAGCCGGGTGGGAAAGATCAC 780
QY 968 GATTACACCAAGTGAACACCTTGCTAGTTGCTAATACGCGCAATTTATTTCTACAA 1027
DB 781 GATTACACCAAGTGAACACCTTGCTAGTTGCTAATACGCGCAATTTATTTCTACAA 840
QY 1028 CGCAGCGCAAGGTTGCCCGAGCCCGCACCCCGTTATTGATTTGATCAAGACGCG 1087
DB 841 CGCAGCGCAAGGTTGCCCGAGCCCGCACCCCGTTATTGATTTGATCAAGACGCG 900
QY 1088 TTGACGCCCATCCACCGCAAAAACAGGCGTATGATGATTAACCACTTCACTGCTG 1147
DB 901 TTGACGCCCATCCACCGCAAAAACAGGCGTATGATGATTAACCACTTCACTGCTG 960
QY 1148 TTTATTCGCGGACAGCATTAATCTGCAAAATCTCGCGCGGCACTGAGCTCACTGCG 1207
DB 961 TTTATTCGCGGACAGCATTAATCTGCAAAATCTCGCGCGGCACTGAGCTCACTGCG 1020
QY 1208 ACGCTTCCCGGTCAAGCGGATTAACAGCGCGTATGATGATTAACCACTTCACTGCTG 1267
DB 1021 ACGCTTCCCGGTCAAGCGGATTAACAGCGCGTATGATGATTAACCACTTCACTGCTG 1080
QY 1268 CGTGGCTTAAGGATTAACAGCGCGTATGATGATTAACCACTTCACTGCTGCTTACG 1327
DB 1081 CGTGGCTTAAGGATTAACAGCGCGTATGATGATTAACCACTTCACTGCTGCTTACG 1140
QY 1328 CAGATCCGATTAACAGCGCGTATGATGATTAACCACTTCACTGCTGCTTACG 1387
DB 1141 CAGATCCGATTAACAGCGCGTATGATGATTAACCACTTCACTGCTGCTTACG 1200
QY 1388 CTGGCAGATGTGAAGAGGAATCGCAGGCGATGTGCTTGGCAGGTTTACGCA 1447
DB 1201 CTGGCAGATGTGAAGAGGAATCGCAGGCGATGTGCTTGGCAGGTTTACGCA 1260
QY 1448 ATCTGGAATGAAGCAGCTTACCGCGCTGCACTTTGTAAT 1487
DB 1261 ATCTGGAATGAAGCAGCTTACCGCGCTGCACTTTGTAAT 1300

RESULT 14
US-10-156-660-1
; Sequence 1, Application US/10156660
; Publication No. US20030103958A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Kretz, Keith
; APPLICANT: Gray, Kevin A.
; APPLICANT: Barton, Nelson R.
; APPLICANT: Garrett, James B.
; APPLICANT: O'Donoghue, Eileen
; TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: AND METHODS FOR MAKING AND USING THEM
; CURRENT APPLICATION NUMBER: US/10/156,660

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CURRENT FILING DATE: 2002-10-01
 PRIOR APPLICATION NUMBER: US 09/866,379
 PRIOR FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: US 09/580,515
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: US 09/318,528
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: US 09/291,931
 PRIOR FILING DATE: 1999-04-13
 PRIOR APPLICATION NUMBER: US 09/259,214
 PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: US 08/910,798
 PRIOR FILING DATE: 1997-08-13
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1308
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: modified phytase enzyme.
 NAME/KEY: CDS
 LOCATION: (1)...(1308)
 US-10-156-660-1

Query Match 66.5%; Score 1263.8; DB 15; Length 1308;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

188 ATGAAGGAGCTTATATCCATTTTATCTTCCTGATTCGTTAACCCGCAATCGCA 247
 1 ATGAAGGAGCTTATATCCATTTTATCTTCCTGATTCGTTAACCCGCAATCGCA 60
 248 TTCGCTCAGAGTGAAGCTGAAAGTGAATGTGATGTGATGTGATGTGATGTGAT 307
 61 TTCGCTCAGAGTGAAGCTGAAAGTGAATGTGATGTGATGTGATGTGATGTGATGTGAT 120
 308 GTGCTGTCTCCACCAAGGCCACGCACTGATGACGATGTGATGATGATGATGATGATGAT 367
 121 GTGCTGTCTCCACCAAGGCCACGCACTGATGACGATGTGATGATGATGATGATGATGAT 180
 368 ACCTGGCCGCTTAACTGGTGTGCTGACACCGCGAGTGTGATGATGATGATGATGATGAT 427
 181 ACCTGGCCGCTTAACTGGTGTGCTGACACCGCGAGTGTGATGATGATGATGATGATGAT 240
 428 GACATTAACCAAGCCGCTGTGCTGACACCGCGAGTGTGATGATGATGATGATGATGAT 487
 241 GACATTAACCAAGCCGCTGTGCTGACACCGCGAGTGTGATGATGATGATGATGATGAT 300
 488 CAGTGTGCTGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
 301 CAGTGTGCTGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 548 GCTTGTGCTGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
 361 GCTTGTGCTGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 608 TCCATCCGATCCGCTTATTTATCTCTTAAATAATGGCGTTTGGCACTGATGATGATGATGAT 667
 421 TCCATCCGATCCGCTTATTTATCTCTTAAATAATGGCGTTTGGCACTGATGATGATGATGAT 480
 668 AACGTGACTGACGCTCTGACGAGGCGAGAGGATGATGATGATGATGATGATGATGATGAT 727
 481 AACGTGACTGACGCTCTGACGAGGCGAGAGGATGATGATGATGATGATGATGATGATGAT 540
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 541 TATCAAAAGCGCTTTCGCAACTGGAAGCGGCTTATTTTCCGCATGCAACTGGGCG 600
 788 CTTAAAGCGTGAAGAACAGAGCAAGCTGTTCATTAGCAGGCAATTACATCGGACTC 847
 601 CTTAAAGCGTGAAGAACAGAGCAAGCTGTTCATTAGCAGGCAATTACATCGGACTC 660

848 AAGTGAAGCGCCGACATGCTCATTAAACGGTGGTGAAGCTTCGATCAATGTGACG 907
 661 AAGTGAAGCGCCGACATGCTCATTAAACGGTGGTGAAGCTTCGATCAATGTGACG 720
 908 GAGATTTTCTCTCTGCAACAGCAAGGATGCGGAGCCGGGTGGGAAAGATGAC 967
 721 GAGATTTTCTCTCTGCAACAGCAAGGATGCGGAGCCGGGTGGGAAAGATGAC 780
 968 GATTACACCAAGTGAACACTTGTGAATTTGATTAAGCGCAATTTTATTTGACAA 1027
 781 GATTACACCAAGTGAACACTTGTGAATTTGATTAAGCGCAATTTTATTTGACAA 840
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 841 CGCAGCCGAGAGTGTGCGGCGACCGCCGACCCGTTATTAATTTGATTAAGCGCA 900
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 1148 TTATGCGCGACACGATTAATCTGCAATCTGCGGCGGCACTGAGCTCAACTGG 1207
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 1448 ATCGTAATGAAGACGATTAACAGCGGATTAACAGCGGATTAACAGCGGATTAAC 1487
 1261 ATCGTAATGAAGACGATTAACAGCGGATTAACAGCGGATTAACAGCGGATTAAC 1300

RESULT 15

US-10-334-672-4
 Sequence 4, Application US/10334672
 Publication No. US20030157646A1
 GENERAL INFORMATION:
 APPLICANT: Lannan, Mike
 APPLICANT: Koepf, Edward
 TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed
 FILE REFERENCE: SYNG-P01-001
 CURRENT APPLICATION NUMBER: US/10/334,672
 PRIOR APPLICATION NUMBER: 60/344,523
 PRIOR FILING DATE: 2001-12-28
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patent version 3.1
 SEQ ID NO 4
 LENGTH: 1281
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: No. US20030157646A19X gene
 US-10-334-672-4

Query Match 35.2%; Score 669.6; DB 15; Length 1281;
 Best Local Similarity 71.3%; Pred. No. 1;le-220;
 Matches 882; Conservative 0; Mismatches 355; Indels 0; Gaps 0;

Tue May 4 07:05:30 2004

us-09-866-379d-7.rnpb

Page 16

QY 251 GCTCAGATGAGCCGAGCTGAGAGCTGAGAAAGTGTGATTTGTCACTGCTCATGTGTG 310
Db 28 GCTCAATCTGAAACAGAAATGAAATGTAATCTGTGTCAATGTCTTCCAAACAGCGGTG 87
QY 311 CGTCTCAGCAACAGGCGAGCAAGCTGATGAGGATGTCAACCCAGAGCGATGAGCCAGC 370
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QY 371 TGCGCGGTAAACTGCGTGTGCTGACACCGCGAGTGTGAGCTAATGCTTATCTGGA 430
Db 148 TGGCTGTGTAAGTTGGGTGAATGATCTCAAGAGGTGTGATTTGATTGCTTACTTGGGT 207
QY 431 CATTAACCAAGCCGAGCTGTGTGAGCCGAGATTTGCTGCGAAAGAGGCTGCGCGAG 490
Db 208 CACTACTGAGAGCAAAAGATTGTGTGTGATGTGTGCTTAAAGTGTGTGCTTCCAA 267
QY 491 TCTGGTCAGTGTGCGATTAATGCTGATGTGACGAGCGTACCCGTAAGAGCGAGCC 550
Db 268 TCTGTGTAAGTTGCTATCATGTGATGTGATGAAAGAACTAGAAAGCTGTGAGAGCC 327
QY 551 TTGCGCGCGCGCTGAGCACTGATGTGCAATTAACGTAATACCGAGAGATAGTCC 610
Db 328 TTGCTGTGCGGTGTGCGCGCGAGCTGTGCTATCACTGTTCACACTCAAGCTGATCTCC 387
QY 611 AGTCCCGATCGGTATTTAATCTCTCTAATAACTGCGCTTGCCTCACTGATTAACGCGAG 670
Db 388 TCTCCAGATCATGTGTCAACCTCATGAGACTGTGTGTCTGATTTGATTAACGCTAAC 447
QY 671 GTGACTGACGAGATCTTCAAGAGGAGAGGCTCAATGTGATTTTACCGGAGATCGG 730
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Db 808 ACTCCAGAGGTGTGAGATTCAGAGCTACTCATTTGTGATGATCAAGACCGCTTGG 867
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Db 868 ACTCCAGAGCGCAAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 927
QY 1151 ATGCGCGAGCAAGATTAATCTGCAATCTGCGAGCGAGCACTGAGCTCACTGAGAG 1210
Db 928 ATGCGCGAGCAAGATTAATCTGCAATCTGCGAGCGAGCACTGAGCTCACTGAGAG 987
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Db 1048 CGACTGTGTGATTAATCTCAATGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1107

QY 1331 ATGCGGATTAAGCGCGCTGTGATTAATGAGCGCGCGAGAGTGAATGAGCCCTG 1390
Db 1108 ATGAGAGCAAGACTCTCAATTTGTCTTGAACCTCAACAGGTGAGTCAAGTTGACCTTG 1167
QY 1391 GCAAGATGTGAAGAGCGAATGCGAGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTG 1450
Db 1168 GCTGTGTGAAAGAAAGAAAGCGTCAAGGTATGTGTGTGTGTGTGTGTGTGTGTGTGTG 1227
QY 1451 GTGAATGAAGCAAGCATACCGCGCTGAGTGTGTAT 1487
Db 1228 GTCAAGAGCGAGATCCAGCTTGTCTTGTAT 1264

Search completed: May 2, 2004, 00:50:59
Job time : 778.893 secs

Db 355 ATGCGCAACTGGCGGTAATACTGGCTGACACACGCGGTGAGTAAATCGC 414
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 Db 415 CTATCTCGGAGATTACCAACGCGCAAGCTCTGGTAGCCGAGATTTGTCGCAAAAAGG 474
 QY 481 CTGCCCCGAGTCTGATCGAGTGGCATTTATGCTGATGTCGACGAGCTACCCGTAAC 540
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 QY 601 AGATACGTCCAGTCCCGATCCGTTATTTATCTCTTAATAAATCGCGCTTTCGCACTGGA 660
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 QY 721 CGGCGATCGGCAAAAGCGCGTTTCGGAATCGGAACGCGTGTCTAATTTCCGCAATCAA 780
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 QY 901 GCTGACGAGATATTTCTCTGCAACAACGCAAGGAATGCCGAGCCGCGGTGGGAAAG 960
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RESULT 2
 US-09-259-214-1
 ; Sequence 1, Application US/09259214A
 ; Patent No. 6110719
 ; GENERAL INFORMATION:
 ; APPLICANT: Kretz, Keith
 ; TITLE OF INVENTION: NOVEL PHYTASE
 ; FILE REFERENCE: DIVER1370-1
 ; CURRENT APPLICATION NUMBER: US/09/259,214A
 ; EARLIER FILING DATE: 1998-03-01
 ; EARLIER APPLICATION NUMBER: 08/910,798
 ; EARLIER FILING DATE: 1997-08-13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1323
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1320)
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(1323)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-259-214-1
 Query Match 67.7%; Score 1287.8; DB 3; Length 1323;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1233; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 188 ATGAAGCGATCTTAATCCCATTTTATCTCTTGATTCCTGTAACCCCGAATCTGCA 247
 Db 1 ATGAAGCGATCTTAATCCCATTTTATCTCTTGATTCCTGTAACCCCGAATCTGCA 60
 QY 248 TTGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTGATTTGATGATGATGAT 307
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 QY 308 GTGCGTCTTCAACCAAGGCGCAACGCACTGATGCGAGATGTACCCGAGCGATGGCA 367
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 QY 548 GCTTTCGCGCGCGGCTGCGACCTTAATGCTGATTAACCGTAAACCGGAGCAATACG 607
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 QY 668 AACGTACTGACGCGATCTCTGACAGGCGAGAGGCTCAATTTGCTGACTTTACCGGCGAT 727
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 QY 788 CTTAAACGTGAGAAACAGAGCAAAAGCTGTTCAATTAACGAGGCAATTAACATGGAATCTC 847

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Db 601 CTTAAAGGTGAGAAACGAGAAAGCTGTTCAATTAGCGAGGATTAACCATCGGAATC 660
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Db 661 AAGGTGAGCGCGCAATGTTCTCATTTAACGGTGGGTAAAGCTTCGATCAATGCTAGC 720
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Db 841 CGCAGCGCCAGAGTTGGCCCGAGCGCGCAACCGGTTATTAAGTTGATCAACAGCAGC 900
Qy 1088 TTGACGCCCATTCACACCGCAAAAACAGCGTATGATGATCAATTAACCATTCAGTCTG 1147
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Db 1021 ACGCTCCCGGTCAAGCGGATTAACCGCGCGCATGATGATGATGATGATGATGATGATG 1080
Qy 1268 CGTGGCGTAAAGCAATACAGCAAGTGAATGAGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1327
Db 1081 CGTGGCGTAAAGCAATACAGCAAGTGAATGAGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1328 CAGATGCGGTAAACAGCGCTGCTCAATTAATACCGCGCGCGCATGAGACTCACTG 1387
Db 1141 CAGATGCGGTAAACAGCGCTGCTCAATTAATACCGCGCGCGCATGAGACTCACTG 1200
Qy 1388 CTGGCAGAGTGTGAAGAGCGAATGCGCAGGCGATGTTGCTGGCAGGTTTAAACGCA 1447
Db 1201 CTGGCAGAGTGTGAAGAGCGAATGCGCAGGCGATGTTGCTGGCAGGTTTAAACGCA 1260
Qy 1448 ATCGTGAATGAAGACGATACCGCGCGTGAAT 1487
Db 1261 ATCGTGAATGAAGACGATACCGCGCGTGAAT 1300

```

```

RESULT 3
US-09-318-528-1
; Sequence 1, Application US/09318528
; Patent No. 6183740
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/09/318,528
; EARLIER FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 09/291,931
; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: 08/910,798
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 09/259,214
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)

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; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or G
US-09-318-528-1

Query Match      67.7%; Score 1287.8; DB 3; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 188 ATGAAAGGATTTAATCCCATTTTATCTCTTGATTCCTGTTAACCCCGAATCTGCA 247
Db 1 ATGAAAGGATTTAATCCCATTTTATCTCTTGATTCCTGTTAACCCCGAATCTGCA 60
Qy 248 TTGCGCTCAGAGTGAAGCGCGAGTGAAGCTGAAGATGAGTGAATGATGATGATGATGATG 307
Db 61 TTGCGCTCAGAGTGAAGCGCGAGTGAAGCTGAAGATGAGTGAATGATGATGATGATGATG 120
Qy 308 GTGCGTCTCCAAACCAAGGCAACGCACTGATGAGATGATGATGATGATGATGATGATGATG 367
Db 121 GTGCGTCTCCAAACCAAGGCAACGCACTGATGAGATGATGATGATGATGATGATGATGATG 180
Qy 368 ACGTGGCGGTTAAACTGCGTGTGCTGCAACCGCGAGTGTGAGTGAATGCGCTATCTC 427
Db 181 ACGTGGCGGTTAAACTGCGTGTGCTGCAACCGCGAGTGTGAGTGAATGCGCTATCTC 240
Qy 428 GGCATTTACCAACGCGCAGCGTCTGTAAGCGCAAGATTGCTGGCGCAAAAAGGCTGCCG 487
Db 241 GGCATTTACCAACGCGCAGCGTCTGTAAGCGCAAGATTGCTGGCGCAAAAAGGCTGCCG 300
Qy 488 CAGTCTGCTCAGTGGCGATTTTGTGATGTCAGACGCTGATCCCGTAAACAGGCGCA 547
Db 301 CAGTCTGCTCAGTGGCGATTTTGTGATGTCAGACGCTGATCCCGTAAACAGGCGCA 360
Qy 548 GCCTTCGCGCGCGGCTGGCACTGCTGCAATTAACGTAATACCCAGGAGATACG 607
Db 361 GCCTTCGCGCGCGGCTGGCACTGCTGCAATTAACGTAATACCCAGGAGATACG 420
Qy 608 TCGATGCCGATCGGTTAATTTATCTCTTAAACCTGCGCTTTGCAACTGATTAACGCG 667
Db 421 TCGATGCCGATCGGTTAATTTATCTCTTAAACCTGCGCTTTGCAACTGATTAACGCG 480
Qy 668 AACGTGATGAGCGCATCTCTGAGGCGAGAGGATCAATGCTGATTAACGCGCAT 727
Db 481 AACGTGATGAGCGCATCTCTGAGGCGAGAGGATCAATGCTGATTAACGCGCAT 540
Qy 728 CGGCAACCGCGTTTCGCAACTGGAACGGGTCTTAATTTTCGCAATCAAACTTGTGC 787
Db 541 CGGCAACCGCGTTTCGCAACTGGAACGGGTCTTAATTTTCGCAATCAAACTTGTGC 600
Qy 788 CTTAAACGTGAAGAACAGGAGAGCTGTTCAATTAACGCGGATTAACCATCGGAATC 847
Db 601 CTTAAACGTGAAGAACAGGAGAGCTGTTCAATTAACGCGGATTAACCATCGGAATC 660
Qy 848 AAGGTGAGCGCGCAATGTTCTCATTTAACGGTGGGTAAAGCTTCGATCAATGCTAGC 907
Db 661 AAGGTGAGCGCGCAATGTTCTCATTTAACGGTGGGTAAAGCTTCGATCAATGCTAGC 720
Qy 908 GAGATATTTCTCCGCAACAGACAGAGGAATGCGAGCGGGGTGGGGAAGATGACC 967
Db 721 GAGATATTTCTCCGCAACAGACAGAGGAATGCGAGCGGGGTGGGGAAGATGACC 780
Qy 968 GATTCAACACAGTGAACACCTTGCTAAAGTTGCATAACCGCAATTTATTTGCTACAA 1027
Db 781 GATTCAACACAGTGAACACCTTGCTAAAGTTGCATAACCGCAATTTATTTGCTACAA 840
Qy 1028 CGCAGCGCCAGAGTTGGCCCGAGCGCGCAACCGGTTATTAAGTTGATCAACAGCAGC 1087
Db 841 CGCAGCGCCAGAGTTGGCCCGAGCGCGCAACCGGTTATTAAGTTGATCAACAGCAGC 900
Qy 1088 TTGACGCCCATTCACACCGCAAAAACAGCGTATGATGATGATGATGATGATGATGATGATG 1147
Db 901 TTGACGCCCATTCACACCGCAAAAACAGCGTATGATGATGATGATGATGATGATGATGATG 960

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QY 1148 TTTATGCGCGGACAGATATCTAATCTGCGAAATCTCGCGCGGCGACTGAGCTCAACTG 1207
Db 961 TTTATGCGCGGACAGATATCTAATCTGCGAAATCTCGCGCGGCGACTGAGCTCAACTG 1020
QY 1208 AGCGTTCGCGGACAGGATTAACAGCGCGGCGGATGTAAGTGTGTTGAAGCTG 1267
Db 1021 AGCGTTCGCGGACAGGATTAACAGCGCGGCGGATGTAAGTGTGTTGAAGCTG 1080
QY 1268 CGTGGCTTAAGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1327
Db 1081 CGTGGCTTAAGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1140
QY 1328 CAGATGCGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1387
Db 1141 CAGATGCGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1200
QY 1388 CTGGCAGATGTAAGGAGGAAATGCGAGGCGATGTTGTTGCGAGTTTAAAGCA 1447
Db 1201 CTGGCAGATGTAAGGAGGAAATGCGAGGCGATGTTGTTGCGAGTTTAAAGCA 1260
QY 1448 ATCGTAATGAAGCAGCATACGGCGTGCAGTTGTAAT 1487
Db 1261 ATCGTAATGAAGCAGCATACGGCGTGCAGTTGTAAT 1300

RESULT 4
US-09-291-931-1
/ Sequence 1, Application US/09291931A
/ Patent No. 6180897
/ GENERAL INFORMATION:
/ APPLICANT: Kretz, Keith
/ TITLE OF INVENTION: NOVEL PHYTASE
/ FILE REFERENCE: 09010/029003
/ CURRENT APPLICATION NUMBER: US/09/291,931A
/ EARLIER FILING DATE: 1999-04-13
/ EARLIER APPLICATION NUMBER: 08/910,798
/ EARLIER FILING DATE: 1997-08-13
/ EARLIER APPLICATION NUMBER: 09/259,214
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1323
/ TYPE: DNA
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1320)
/ NAME/KEY: misc. feature
/ LOCATION: (1)...(1323)
/ OTHER INFORMATION: n = A,T,C or G
US-09-291-931-1

Query Match 67.7%; Score 1287.8; DB 3; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 188 ATGAAGGATCTTAATCCATTTTATCTCTTCTGATTCGGTTAAACCCCGCATCTGCA 247
Db 1 ATGAAGGATCTTAATCCATTTTATCTCTTCTGATTCGGTTAAACCCCGCATCTGCA 60
QY 248 TTCGCTCAGAGTGAACCGGAGCTGAAGTGAAGTGTGATTTGTCAGTCTCATGCT 307
Db 61 TTCGCTCAGAGTGAACCGGAGCTGAAGTGTGATTTGTCAGTCTCATGCT 120
QY 308 GTGCGTGTCTCCAAACCAAGGCGCAAGTGAATGTCACCCCGAGAGCTGCGCA 367
Db 121 GTGCGTGTCTCCAAACCAAGGCGCAAGTGAATGTCACCCCGAGAGCTGCGCA 180
QY 368 ACCTGCGCGGTAAACTGCGTGTGCTGACACCGCGAGGTGATGATGCTATCTC 427
Db 181 ACCTGCGCGGTAAACTGCGTGTGCTGACACCGCGAGGTGATGATGCTATCTC 240

QY 428 GGAATATTACCAACGCGAGCTGTGTAAGCCGACGATTTGCTGCGAAAAAGGCTGCGCG 487
Db 241 GGAATATTACCAACGCGAGCTGTGTAAGCCGACGATTTGCTGCGAAAAAGGCTGCGCG 300
QY 488 CAGTCTGTGAGGTGCGGATTTATGCTGATGTCAGAGCGATACCGGTAAACAGGCGAA 547
Db 301 CAGTCTGTGAGGTGCGGATTTATGCTGATGTCAGAGCGATACCGGTAAACAGGCGAA 360
QY 548 GCCTTGCAGCGCGGCTGCGACCTGACCTGACATTAACCGTACATACCGGAGATAG 607
Db 361 GCCTTGCAGCGCGGCTGCGACCTGACCTGACATTAACCGTACATACCGGAGATAG 420
QY 608 TCCAGTCCCGATACCGGATTTATGCTGATGTCAGAGCGATACCGGTAAACAGGCGAA 667
Db 421 TCCAGTCCCGATACCGGATTTATGCTGATGTCAGAGCGATACCGGTAAACAGGCGAA 480
QY 668 AACGTGATGACCGGATCTCTGACAGGCGAGGATGATGATGATGATGATGATGATGAT 727
Db 481 AACGTGATGACCGGATCTCTGACAGGCGAGGATGATGATGATGATGATGATGATGAT 540
QY 728 CCGCAACCGGCTTTGCGCACTGGAACGGGTGCTTAATTTCCGCAATCAACTTGTGCG 787
Db 541 CCGCAACCGGCTTTGCGCACTGGAACGGGTGCTTAATTTCCGCAATCAACTTGTGCG 600
QY 788 CTTAAACGTGAGAAACAGGACGAAAGCTGTCATTACGAGGATTAACATCGGAACTC 847
Db 601 CTTAAACGTGAGAAACAGGACGAAAGCTGTCATTACGAGGATTAACATCGGAACTC 660
QY 848 AAGTGAAGCGCGCAATGCTCTCATTAACCGGTGCGATGATGCTGATGATGCTGATG 907
Db 661 AAGTGAAGCGCGCAATGCTCTCATTAACCGGTGCGATGATGCTGATGATGCTGATG 720
QY 908 GAGATATTTCTCTGCAACAGCAAGGATGCGGAGCGGCGGATGCGGAGGAGATCACC 967
Db 721 GAGATATTTCTCTGCAACAGCAAGGATGCGGAGCGGAGGATGCGGAGGAGATCACC 780
QY 968 GATTCAACCGAGTGAACACCTTGCTGATGATGATGATGATGATGATGATGATGATG 1027
Db 781 GATTCAACCGAGTGAACACCTTGCTGATGATGATGATGATGATGATGATGATGATG 840
QY 1028 CGGAGCGCGAGGTTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1087
Db 841 CGGAGCGCGAGGTTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
QY 1088 TTGACGCGCCCATTCACCGGAAACAGGCGTATGATGATGATGATGATGATGATGATG 1147
Db 901 TTGACGCGCCCATTCACCGGAAACAGGCGTATGATGATGATGATGATGATGATGATG 960
QY 1148 TTTATGCGCGGACAGATATCTAATCTGCGAAATCTCGCGCGGCGACTGAGCTCAACTG 1207
Db 961 TTTATGCGCGGACAGATATCTAATCTGCGAAATCTCGCGCGGCGACTGAGCTCAACTG 1020
QY 1208 AGCGTTCGCGGACAGGATTAACAGCGCGGCGGATGTAAGTGTGTTGAAGCTG 1267
Db 1021 AGCGTTCGCGGACAGGATTAACAGCGCGGCGGATGTAAGTGTGTTGAAGCTG 1080
QY 1268 CGTGGCTTAAGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1327
Db 1081 CGTGGCTTAAGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1140
QY 1328 CAGATGCGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1387
Db 1141 CAGATGCGGATTAACAGCGGATGTAAGTGTGTTGAAGCTG 1200
QY 1388 CTGGCAGATGTAAGGAGGAAATGCGAGGCGATGTTGTTGCGAGTTTAAAGCA 1447
Db 1201 CTGGCAGATGTAAGGAGGAAATGCGAGGCGATGTTGTTGCGAGTTTAAAGCA 1260
QY 1448 ATCGTAATGAAGCAGCATACGGCGTGCAGTTGTAAT 1487
Db 1261 ATCGTAATGAAGCAGCATACGGCGTGCAGTTGTAAT 1300

RESULT 5
 US-08-910-798-1
 ; Sequence 1, Application US/08910798
 ; Patent No. 5876997
 ; GENERAL INFORMATION:
 ; APPLICANT: KREITZ
 ; TITLE OF INVENTION: NOVEL PHYTASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,798
 ; FILING DATE: August 13, 1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HAILE, PH.D., LISA A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 09010/029001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1272 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; IMMEDIATE SOURCE:
 ; CLONE: PHYTASE
 ; FEATURE:
 ; NAME/KEY:
 ; LOCATION:
 ; US-08-910-798-1

Query Match 61.9%; Score 1175.8; DB 2; Length 1272;
 Best Local Similarity 95.5%; Pred. No. 0;
 Matches 1242; Conservative 0; Mismatches 7; Indels 51; Gaps 1;

QY 188 ATGAAGCGATCTTATCCCATTTTATCTCTTGATTCGGTTAAACCCCGCAATCTGA 247
 DB 1 ATGAAGCGATCTTATCCCATTTTATCTCTTGATTCGGTTAAACCCCGCAATCTGA 60
 QY 248 TTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTGATGTCACTGCTGATGAT 307
 DB 61 TTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTGATGTCACTGCTGATGAT 120
 QY 308 GTTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTCACTGCTGATGATGAT 367
 DB 121 GTTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTCACTGCTGATGATGAT 180
 QY 368 ACCTGCGCGGTAAATCTGGTGTGCTGACACCGCGGTGTGAGTAACTGCTATCTC 427
 DB 181 ACCTGCGCGGTAAATCTGGTGTGCTGACACCGCGGTGTGAGTAACTGCTATCTC 240
 QY 428 GGAATTAACCAATGCGATGCTGTGTAACCGCAATGCTGCTGCGAATAAGGCTGCGCG 487
 DB 241 GGAATTAACCAATGCGATGCTGTGTAACCGCAATGCTGCTGCGAATAAGGCTGCGCG 300
 QY 488 CAGTGTGTCAGGTCGCGATTAATTTGCTGATGTGACAGAGCTAACCGTTAAACAGGCGAA 547
 DB 301 CAGTGTGTCAGGTCGCGATTAATTTGCTGATGTGACAGAGCTAACCGTTAAACAGG---- 356

QY 548 GCCTGCGCGCGGCTGCGACTGATGTGCAATACCGTACATACCGAGCAGATACG 607
 DB 357 -----CGAGCGAGATACG 369
 QY 608 TCCAGTCCCGATCCGTTATTTAATCCCTAATAAACTGAGGTTTGCCCACTGTATAACGCG 667
 DB 370 TCCAGTCCCGATCCGTTATTTAATCCCTAATAAACTGAGGTTTGCCCACTGTATAACGCG 429
 QY 668 AACGTGACTGACCGCATCTCAAGAGGCGAGAGGCTCAATTGCTGACTTTACCGGCGAT 727
 DB 430 AACGTGACTGACCGCATCTCAAGAGGCGAGAGGCTCAATTGCTGACTTTACCGGCGAT 489
 QY 728 CCGCAAAACGCGGTTTGCGCAACTGGAACGGGTCTTAATTTTCCGCAATCAACTGTGCG 787
 DB 490 CCGCAAAACGCGGTTTGCGCAACTGGAACGGGTCTTAATTTTCCGCAATCAACTGTGCG 549
 QY 788 CTTAAACGTGAGAAACAGACGAAGCTGTTCAATTAACGAGCATTAATCCATCGAACTC 847
 DB 550 CTTAAACGTGAGAAACAGACGAAGCTGTTCAATTAACGAGCATTAATCCATCGAACTC 609
 QY 848 AAGGTGAGCGCGCAATGCTCATTTAACCGGTGAGTAAAGCTCGCATTAATGCTGAGCG 907
 DB 610 AAGGTGAGCGCGCAATGCTCATTTAACCGGTGAGTAAAGCTCGCATTAATGCTGAGCG 669
 QY 908 GAGATATTTCTCTGCAACAGCAACGGAATCCGAGCCGCGGTGAGGAGAGATCACG 967
 DB 670 GAGATATTTCTCTGCAACAGCAACGGAATCCGAGCCGCGGTGAGGAGAGATCACG 729
 QY 968 GATTCAACAGAGTGAACACCTTGTCAATTTGCTGATTAACCGCAATTTATTTTGCTACAA 1027
 DB 730 GATTCAACAGAGTGAACACCTTGTCAATTTGCTGATTAACCGCAATTTATTTTGCTACAA 789
 QY 1028 CGCAGCGCAGAGGTTGCGCCAGCCGCGCAACCCGTTATTAATTTGATCAAGACAGCG 1087
 DB 790 CGCAGCGCAGAGGTTGCGCCAGCCGCGCAACCCGTTATTAATTTGATCAAGACAGCG 849
 QY 1088 TTGAGCGCCCATCCATCCAGCAAAAACAGGCGTATGCTGACATTAACCACTTCAGTCTG 1147
 DB 850 TTGAGCGCCCATCCATCCAGCAAAAACAGGCGTATGCTGACATTAACCACTTCAGTCTG 909
 QY 1148 TTATGCGCGGAGACGATATCAATCTGCAAAATCTCGCGCGGCGCATGAGCTCAACTCG 1207
 DB 910 TTATGCGCGGAGACGATATCAATCTGCAAAATCTCGCGCGGCGCATGAGCTCAACTCG 969
 QY 1208 ACCTTCCTCCGATCAGCCGATTAACAGCGCCGCGAGTGTGATCTGTGTTGAACGCTCG 1267
 DB 970 ACCTTCCTCCGATCAGCCGATTAACAGCGCCGCGAGTGTGATCTGTGTTGAACGCTCG 1029
 QY 1268 CGTGGGCTAAGCGTAAACAGCAAGTGAATTCAGGTTTCGCTGCTCCAGACTTTACAG 1327
 DB 1030 CGTGGGCTAAGCGTAAACAGCAAGTGAATTCAGGTTTCGCTGCTCCAGACTTTACAG 1089
 QY 1328 CAGATGCGGTATAAAGCGCGCTGTCTAATTAATACGCGCGCGAGAGTGAATCTGACC 1387
 DB 1090 CAGATGCGGTATAAAGCGCGCTGTCTAATTAATACGCGCGCGAGAGTGAATCTGACC 1149
 QY 1388 CTGGCAGAGTGTGAAGAGCAATAGCGCAGGAGATGTTGCTGTTGAGAGTTTATCGCAA 1447
 DB 1150 CTGGCAGAGTGTGAAGAGCAATAGCGCAGGAGATGTTGCTGTTGAGAGTTTATCGCAA 1209
 QY 1448 ATCGTGAATGAAGACGATACCGGCGCTGCAATTTGTAAT 1487
 DB 1210 ATCGTGAATGAAGACGATACCGGCGCTGCAATTTGTAAT 1249

RESULT 6
 US-09-489-940/C
 ; Sequence 940, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

```

1 FILE REFERENCE: 2709.2004001
2 CURRENT APPLICATION NUMBER: US/09/469,039A
3 CURRENT FILING DATE: 2000-01-27
4 PRIOR APPLICATION NUMBER: US 60/117,747
5 PRIORITY FILING DATE: 1999-01-29
6 NUMBER OF SEQ ID NOS: 14342
7 SEQ ID NO 940
8 LENGTH: 2226
9 TYPE: DNA
10 ORGANISM: Klebsiella pneumoniae
11 US-09-469-039A-940

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	Query Match	6.3%;	Score 120.2;	DB 4;	Length 2226;	
	Best Local Similarity	63.1%;	Pred. No. 3.8e-28;			
	Matches 185;	Conservative 0;	Mismatches 109;	Indels 0;	Gaps 0;	
QY	1555	TCAGTTTCCCTCTTCTTCGTAGACTATTAACCGGAATAAGTTAATAGCCGTAACTGTAGC	1654			
Db	2226	TTAATCGGTTTTTTTATCAGATAAGAATAAACCAATAAGTTATAGCATAGCCATAATA	2167			
QY	1655	GATGCTGGCGGTTTATATCACACCATTAGATAGCGCTTTAATATTAGCGCTGCCTG	1714			
Db	2166	GOTGTACCCCTTTTCAACGACGCCATTAGAATACAGCCTTTTACAATTAACCACTTTG	2107			
QY	1715	TTCCGAAGCTTGCACTTAGCAAACTACCTCTTTGGCGGTGTTCMAAGCAAAGCGGCAC	1774			
Db	2106	TTCAATATGCTTCACACTAATCACTTCAATTTCTTGCAGATATTTCTTCAAGCGGCAC	2047			
QY	1775	CAGCAGCGTGTGCCACAGAACGCCCCACGACCGCGGATCTACACCGCCAGCATGG	1834			
Db	2046	CAATAAAGATGTACAGCATTAACGACCAATGATTCACACATGGTAACAGCCAAATGG	1987			
QY	1835	CGGCGTATCGCAATCACACAGATGCTAANGCTGTCCCACTTCAGTAANT	1887			
Db	1986	TGGAATATCGAAGATTAATTAATCAATAACTGAAGTGGCCATTTTAATAATT	1934			

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RESULT 7
US-09-328-352-1473/c
; Sequence 1473, Application US/09328352
; Patent No. 6562858
; GENERAL INFORMATION:
; APPLICANT: Gary L. Brelton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC09-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1473
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1473

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Query Match	3.9%	Score 73.2	DB 4	Length 2202
Best Local Similarity	55.9%	Pred. No. 5	7e-13	
Matches 160	Conservative 0	Mismatches 123	Indels 3	Gaps 1
QY	1602	TCCTCTTTCTCGAGTAATAAACCGRATATAGTATAGCCGTAACTGTAAAGCGGTCTG	1662	
Db	2198	TCCTCTTTTGTGCGTTATAGGCATTAAGCATAGTATATACCAATACATAGCAAGCAGCTA	2133	
QY	1662	GCGCGTTATATACACCATTTGAGATAGCGCCTTTATATATGACGCGCTGCTGTCCAGA	1721	
Db	2138	GCACGTTGAT--ATCATTTAGAAATTAAGCCGTTGACTTAACTCCGCGCTGTCCAAA	2082	
QY	1722	CGCTGCATTTGACAAACTCACCTTTTGGGGGTCTCAACCCAAAACGGCCAAACCGAGG	1783	
Db	2081	CGGTAAAGGTATATCAAGTCTTTTATCTGAGATTAGCAATTAAGCGCCAACTTAAG	2022	
QY	1783	CTGGTGCACACGAACGCCCAAGACCGGGGATCATCTACCGCAGCATCGCGCGCTTA	1841	

Db 2021 TTCACACCGGTTATTTGGAAATATATATACACCGGTTACTGCAAGTCTGTTGGAGTA 1962

Qy 1842 TCGACATCACAGATCGTATGCTGCTGGCCATTCAGTATT 1887

Dd 1961 TCATATATGATGTGTCATATTGGCTTTGAGCTGCTCAAGTATT 1916

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RESULT 8
US-09-489-039A-341
; Sequence 341, Application US/09489039A
; Patent No. 6610636
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 341
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-341

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Query March	3.3%	Score 63.6	DB 4	Length 1266
Best Local Similarity	48.7%	Pred. No. 5.2e-10		
Matches 202	Conservative 0	Mismatches 210	Indels 3	Gaps 1
QY	273	AGCTGAAAAGTGTGATTTGTCACTGCTCATGCTGTGCGTCTCC---AACCAAGGCCA	329	
Db	113	AGCTGACGAGGAGTGCTGATCATGAGCCCTCAACACGTCGTGGCGCTTGGCCAAATPAG	172	
QY	330	CGCAACTGATGACGAGATGTCAACCCGACGCAATGACCAACTGACCGGTTAACTGGT	389	
Db	173	GCAAGCGCTTGAACACGTCCACCGCCAAAGGCTTGCCCGCAGTGAATGTCCGGGGGCC	232	
QY	390	GAGTGCACACCGCGAGTGTGTAGCTAATCGCTATCTCGACATTAACAACGCAAGCTC	449	
Db	233	AGCTGACACCAAAAGCCGTTGTGTGAGAGTGTATATGGGCACTATATGCGGAATGAGC	292	
QY	450	TGTTGACCGACGAGATTGCTGCGAAAAAGGCTCCCGCACTCTGGTCAGTGGCGATTA	509	
Db	293	TGGCGACGACGAAGCTGTGTGACCAACGGCGAGTCCCGCGGAAACCGCGTTTATGCTT	352	
QY	510	TTGTGTATGTGACGACGACGTACCCGTTAAACAGCGCAAGCTTTCGCCCGCGACTGGCAC	569	
Db	353	ACGCTTAACAGCTCGACGCGCACCGTCCGACACCGGCACTTTTATACCGGGGCGTTC	412	
QY	570	CTGACTGTGCATTAACCGTACATACCAACGAGATATAGTCACTCCCGATCCGTTATTTA	629	
Db	413	CGGGCTGCGGCACATCCGGGTGATCACGAGCTCATGATGGGACCATGAAACCGACCTTCA	472	
QY	630	ATCTCTAAATAATGGCGTTTGGCAACTGATTAACGGAACGTACATGACGCGAT	684	
Db	473	ACCGGTTATTAACGACACTCCCGGGGTTTCGCGAAAAAGCGTCCAGAGCAT	527	

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1 RESULT 9
2 US-09-934-899-7/c
3 ; Sequence 7, Application US/09934899
4 ; Patent No. 6537786
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Wang, Siqun
9 ;
10 ; APPLICANT: Wang, Tao
11 ;
12 ; APPLICANT: Kofeae, Mattheos
13 ;
14 ; APPLICANT: Odgom, U. Matlin
15 ;
16 ; APPLICANT: Ye, Rick
17 ;
18 ; TITLE OF INVENTION: Genes encoding exopolysaccharide production
19 ;
20 ; FILE REFERENCE: C11633 US NA
21 ;
22 ; CURRENT APPLICATION NUMBER: US/09/934,899
23 ;

```

Tue May 4 07:05:30 2004

us-09-866-379d-7.rni

Page 7

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? CURRENT FILING DATE: 2001-08-22
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: Microsoft Office 97
? SEQ ID NO 7
? LENGTH: 2337
? TYPE: DNA
? ORGANISM: Methylobionas 16a
US-09-934-899-7

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Query Match	2.9%	Score 55.2	DB 4	Length 2337
Best Local Similarity	50.8%	Pred. No. 3.8e-07		
Matches 132; Conservative	0	Mismatches 128	Indels 0	Gaps 0

QY	1622	ATAACCGTAATAGTATTATAGCGGTACGTATAGACGGGTGCTGGCGGTTTAATCAACCAATT	1661
Db	2205	ATCCCGCTGATAGGCGATAGCCGTAGTACGGGTAATAGACAGAACCTTCTCTCATGTGCTT	2146
QY	1682	GAGGATAGCGCCTTTAATATTAGACGCCCTGCCCTGTTCAGACGCTGCATTGACAACTCAC	1741
Db	2145	GATGATGAAACCGTTGGGTTTCAAGCCGACTTGTGCTCAAGGCGCTGAAACTGACCTCCAG	2086
QY	1742	CTCTTTGGCGGTTGTTCAAGCCAAAACGGCAACGACGCGTGGTGCACATAGAACGCCC	1801
Db	2085	CTCTTGGCGGTTATACGGCCCTCTCTTACACACAGGAAGTAGCATGCATGCTTGC	2026
QY	1802	CACGACCGCGCATCATCTACACCGCAGCATCGCGGCGTATCGACAACTCACACAGTCGTA	1861
Db	2025	CATGATGCGCGCGTGGTGGCGGCCCAAGATCGCGCGGCAATCGATGACGATATGGTGTGA	1966
QY	1862	ATGTCGTTGCGCCATTGCCA	1881
Db	1965	AAAGCTTTCAAGTTGCTCCA	1946

RESULT 10

US-08-956-171E-84/c
; Sequence 84, Application US/08956171E
; Patent No. 6593114

```

;
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;

```

Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: staphylococcus aureus polynucleotides and sequences
NUMBER OF SEQUENCES: 5256

;
;
;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

```
;
; ZIP: 20850
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Diskette, 3.50 inch, 1
; COMPUTER: HP Vectra 486/33

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;
OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
;

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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E

```

;
 FILING DATE: 20-Oct-1997
 ;
 CLASSIFICATION: <Unknown>
 ;

;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
;

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986

FILING DATE: January 3
ATTORNEY/AGENT INFORMATION:

```

; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
;

```

REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 5738 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO. 84

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Query Match      2.7%;      Score 51.4;  DB 4;      Length 5738;
Best Local Similarity 52.0%;  Pred. No. 1, 1e-05;
Matches 115; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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Qy	1680	TTGAGGATAGGCGCTTTAAATATGACGCGCGCTGTTCAGACGCTGATGACAAATC	1739
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Db	838	TTCAAATATGACACTTAAGATGTTACTGCTTCTTTTCATATAGTCTTTTCTTTT	779
Qy	1740	ACCTCTTTGGCGGCTGTCAAGCCAAAACGGCGCAACGACGAGCTGTGCCAACAAAGC	1799
Db	778	ACTTCATTATTATCATTTTTTTTTCATCAATTAATCAACAGATCATTTTAAATGACAGC	719
Qy	1800	CCACGACCGCGGATCACTGACCCGACGATCGCGGCGCTATGACATACACGATCG	1859
Db	718	GCAATATAGTTGTGCATCAGTCACTAGTATTAATCGCGGTGATGAGACATATATATGTCG	659
Qy	1860	TAAATGCTGTTGCGCCATCCAGATTAATGACGATCCGATC	1900
Db	658	TAACTTTATTAACAAGATCACTAATTTCTTTGAACCTTTC	618

RESULT 11

US-09-634-238-28/c
; Sequence 28, Application US/09634238
; Patent No. 6544772

; GENERAL INFORMATION;
; APPLICANT: Glenn,

APPLICANT: Havukkala, Ilkka J.
APPLICANT: Bloksberg, Leonard, N

```

; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James

```

APPLICANT: Christensson, Anna C
; Holland, Ross
; APPLICANT:

; APPLICANT: O'Toole, Paul W
; APPLICANT: Reid, Julian R.

APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating

```

; TITLE OF INVENTION: chem and methods for using chem
; FILE REFERENCE: 11000.1043U1

```

;
CURRENT APPLICATION NUMBER: US/09/634,238
;
CURRENT FILING DATE: 2000-08-08
;

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; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.

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; SEQ ID NO 28
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; LENGTH: 2326

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; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus

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US-09-634-238-28

Query Match
Best Local Sim

Matches 127;

Qy 1631 AT

Db 1937 ATAAccATAgCCATAccGTAGC

1691 GCCTTAATGACGCTGCC

Db 1877 ACCGATATATTTAGCCTGAGCCAAATTTTAAACCTTAACGTTCGACGTAATCTCCCTT 1818
QY 1751 GGTGTTCAAGCCAAACGCGCAACGACGAGCTGGTGCCTCAACAGAACGCCCCACGACCGC 1811

Db	1817	TAATGCTTTCCAAATATTGCGACGACCAACAATCCGCAATTTTGGAACTAATACITG	1758
QY	1811	GGCATCACTACCGCCAGCATCGCGCGTATCGACAATACCGAGATCGTATGCTGTT	1870
Db	1757	AACATAGACACTCTCTAAACTGGTGGGCGCTCAAGAACATATATGTAATTAGACCG	1698
QY	1871	CGCCATTCGAGTAATGAGGCAATCCGAT	1899
Db	1697	AGCCCACTCCACAGTTCCACCATTTGCTT	1669

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RESULT 12
US-09-710-794-4/C
; Sequence 4, Application US/09710794
; Patent No. 6573069
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: NOVEL CRIB PROTEIN ZMS61
; FILE REFERENCE: 99-76
; CURRENT APPLICATION NUMBER: US/09/710,794
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164,685
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4:
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)...(1219)
; US-09-710-794-4

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```

RESULT 13
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6503729
TITLE OF INVENTION: jamaaschi
FILE REFERENCE: FB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA

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ORGANISM: Methanococcus jannaschii	FEATURE:
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LOCATION: (128222)..(128222)	
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LOCATION: (84773)..(84773)	
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NAME/KEY: misc_feature	
LOCATION: (84812)..(84812)	
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NAME/KEY: misc_feature	
LOCATION: (98120)..(98120)	
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NAME/KEY: misc_feature	
LOCATION: (98159)..(98159)	
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NAME/KEY: misc_feature	
LOCATION: (98239)..(98239)	
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NAME/KEY: misc_feature	
LOCATION: (98266)..(98266)	
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NAME/KEY: misc_feature	
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NAME/KEY: misc_feature	
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NAME/KEY: misc_feature	
LOCATION: (305396)..(305396)	
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NAME/KEY: misc_feature	
LOCATION: (309418)..(309418)	
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NAME/KEY: misc_feature	
LOCATION: (312837)..(312837)	
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NAME/KEY: misc_feature	
LOCATION: (312993)..(312993)	
OTHER INFORMATION: n equals a, t, c, or g	
NAME/KEY: misc_feature	
LOCATION: (319226)..(319226)	


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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
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NAME/KEY: misc feature
LOCATION: (657081)..(657081)
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
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NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
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LOCATION: (779455)..(779455)
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LOCATION: (779676)..(779676)
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LOCATION: (871619)..(871619)
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NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1139881)..(1139881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
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NAME/KEY: misc feature
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LOCATION: (1349473)..(1349473)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1565020)..(1565020)
OTHER INFORMATION: n equals a, t, c, or g

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NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

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Query Match 2.0%; Score 38.4; DB 4; Length 1664976;
Best Local Similarity 5.1%; Pred. No. 4.8;
Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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QY 151 ATCATATATGTCAGATATGAAAGCGAAACATATCATGAAAGCGATTTATCCATT 210
Db 1133087 ATCCCTTAATATATATTTATTAATAATTCGGATGAAATTTATCTTCCTTATT 1133146
QY 211 TTATCTCTTCGATTCGTTAACCCCGCATCTGCTCAGAGTGAAGCGAGCT 270
Db 1133147 TTAGCTTTATGATTCATTTTCATTAATATTTAGTAATGAGCGAGCTTATT 1133206
QY 271 GAAGCTGAAGTGTG 286
Db 1133207 AGTTTATGATTAATGTG 1133222

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RESULT 14
US-09-252-991A-11337/c
; Sequence 11337, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OR INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ. ID NOS: 33142
; SEQ. ID NO 11337
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11337

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Query Match 2.0%; Score 37.2; DB 4; Length 1053;
Best Local Similarity 51.9%; Pred. No. 0.16;
Matches 84; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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QY 1718 CAGACGCTGATGACAACTGACCTCTTGGGGGTTCAGACCAAGCGCAACGAG 1777
Db 357 CATGCGCTGATGAAAGAAACCATGCTGTCGACAGCGGAGTGTTCGGCATCA 298
QY 1778 CAGGCTGTGTCGCAAGAAAGCCCAAGACCGGGGATCACTGACCGCAGATCGCGG 1837
Db 297 CAGTCCGGAATCGCCGATCCGAGCGCGGGCGGAGCGCTCGCTCCAGGCTGCGCG 238
QY 1838 CGTATCGAAGATCAACGAGATGTAATGTGCTTCCGCAATC 1879
Db 237 CGGCAAGCGGCTCATGAGGCTGTCCGAGCTGCGCTCCCATC 196

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RESULT 15
US-09-252-991A-11293
; Sequence 11293, Application US/09252991A

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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11293
LENGTH: 2334
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11293

Query Match 2.0%; Score 37.2; DB 4; Length 2334;
Best Local Similarity 51.9%; Pred. No. 0.25; Mismatches 78; Indels 0; Gaps 0;
Matches 84; Conservative 0;

QY	1718	CAGACGCTGATGACAACTCACTCTTTGGCGGTTCAGACCAAAAGCGCAACAG	1777
DB	552	CATGCGCTGGATGAGAAACCATGTGTGTGACAGCGGAGTGGTATCGCGATCCA	611
QY	1778	CAGGCTGTGCGCAACAGAACGCCCCGACCGGCGATCACTACCGCCAGCATCGCGG	1837
DB	612	CAGTCGCGAATCGCCGATCCCGAGCGCGGCGCGCGCTCGCTCCAGCGTGC	671
QY	1838	CGTATCGACATACCGCATCGTATGTGTGCGCCATTC	1879
DB	672	CGGACGCGCGCTCTATCGGCTGTCCGCGTCCCGAGTC	713

Search completed: May 2, 2004, 00:29:07
Job time: 163.653 secs